

#5

SEQUENCE LISTING

<110> University of Utah Research Foundation
Cognetix, Inc.
Olivera, Baldomero M.
Cartier, G. Edward
Watkins, Maren
Hillyard, David R.
McIntosh, J. Michael
Layner, Richard T.
Jones, Robert M.

<20> O-Superfamily Conotoxin Peptides

<130> 2314-227

<140> US 09/749,637

<141> 2000-12-28

<150> US 60/243,412

<151> 2000-10-27

<150> US60/219,440

<151> 2000-07-20

<150> US 60/214,263

<151> 2000-06-26

<150> US 60/173,754

<151> 1999-12-30

<160> 409

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> Conus gloriamaris

<220>

<221> CDS

<222> (1)..(231)

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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag att ctt 96

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
20 25 30

ttt ccg aag gcg ggt cac gaa atg gag aac ctc gaa gtc tct aat cgg 144

Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
35 40 45

gtc aag ccg tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa 192

Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
50 55 60

aac tgc tgc cgt ggc tgg aat tgc gtt ctt ttc tgc gtc tgaaactacc 241

Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
65 70 75



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gtgatgtctt ctctcccctc

261

<210> 2
 <211> 77
 <212> PRT
 <213> Conus gloriamaris

<400> 2
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
 20 25 30
 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
 35 40 45
 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
 50 55 60
 Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
 65 70 75

<210> 3
 <211> 29
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 <213> Conus gloriamaris

<220>
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 <222> (1)..(29)
 <223> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue
 e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
 or bromo-Trp

<400> 3
 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
 1 5 10 15
 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
 20 25

<210> 4
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 <213> Conus gloriamaris

<220>
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 <222> (1)..(29)
 <223> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residu
 e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 15 may be Tyr
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospn
 o-Tyr; Xaa at residue 22 may be Trp or bromo-Trp

<400> 4
 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Xaa Gln
 1 5 10 15
 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
 20 25

<210> 5
 <211> 29

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<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp or bromo-Trp; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 5
Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
1 5 10 15
Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Xaa Cys Val
20 25

<210> 6
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<212> DNA
<213> Conus omaria

<220>
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<222> (146)..(235)

<400> 6
gaagctggta cgcctgcagg taccgggtccg gaattcccgg gtcgacatca tcatcatcga 60
tccatctgtc catccatcca ttcattcatt cgctgccaga ctataataaa cattcaagtc 120
tctctttctt tttgtgtctg acaga tgc atc agg atg tgc cgt aga gaa gct 172
Ser Ile Arg Met Cys Arg Arg Glu Ala
1 5
caa ctt tgt gat ccg att ttt caa aac tgc tgc cat ggc ttg ttt tgc 220
Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys
10 15 20 25
gtt ttg gtc tgc gtc taaaactacc gtgatgtctt ctctctccct ctagtagtag 275
Val Leu Val Cys Val
30
taggcggccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt 335
ctatagtgtc acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa 395
accctggcgt taccctaactt aatcgcttg cagcacatcc ccttttcgcc agctggcgta 455
atagcgaaga ggcccgacc gatcgccctt cccaacagtt ggcgagcctg aatggcgaat 515
gggacgcgcc ctgtagcggc gcattat 542

<210> 7
<211> 30
<212> PRT
<213> Conus omaria

<400> 7
Ser Ile Arg Met Cys Arg Arg Glu Ala Gln Leu Cys Asp Pro Ile Phe
1 5 10 15
Gln Asn Cys Cys His Gly Leu Phe Cys Val Leu Val Cys Val

20 25 30

<210> 8
 <211> 27
 <212> PRT
 <213> Conus omaria

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 5 is Glu or gamma-carboxy-Glu; Xaa at residue 11 may be Pro or hydroxy-Pro

<400> 8
 Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys
 1 5 10 15

Cys His Gly Leu Phe Cys Val Leu Val Cys Val
 20 25

<210> 9
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 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (25)..(315)

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 1 5

gct gtg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gat gac tcc 99
 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser
 10 15 20 25

aga aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag 147
 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu
 30 35 40

aac ctc gaa gac tct aaa cac agg cac cag gag aga ccg gac acc ggc 195
 Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly
 45 50 55

gac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa 243
 Asp Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys
 60 65 70

gaa cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg 291
 Glu His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp
 75 80 85

tat tgc gtt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactcccat 345
 Tyr Cys Val Val Leu Ser Cys Thr
 90 95

c 346

<210> 10
 <211> 97
 <212> PRT
 <213> Conus textile

tgg aca ttc gtc acg gct gat gac tct gga aat gga ttg ggg aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
 20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac aag agg tgc gtt cca cac gag ggc cct tgt aat tgg ctt aca caa 192
 Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
 50 55 60

aac tgc tgc agt ggt tat aat tgc atc att ttt ttc tgc cta 234
 Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu
 65 70 75

taaaactacc gtgatgtctt ctcttcccct c 265

<210> 13
 <211> 78
 <212> PRT
 <213> Conus omaria

<400> 13
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Ser Leu Thr Gly
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
 50 55 60

Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu
 65 70 75

<210> 14
 <211> 27
 <212> PRT
 <213> Conus omaria

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro; Xaa at residue
 5 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Trp
 or bromo-Trp; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 14
 Cys Val Xaa His Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
 1 5 10 15

Ser Gly Xaa Asn Cys Ile Ile Phe Phe Cys Leu
 20 25

<210> 15
 <211> 321
 <212> DNA
 <213> Conus dalli

<220>
 <221> CDS
 <222> (1)..(291)

<400> 15
 atg aaa ctg acg tgc ctg ctg atc att gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Leu Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
 20 25 30

ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45

agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60

cag aga cag gtc aag ccg tgt cgt aaa gaa cat caa ctt tgt gat ctg 240
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
 65 70 75 80

att ttt caa aac tgc tgc cgt ggc tgg tat tgc ttg ctt cgt cct tgc 288
 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys
 85 90 95

atc tgaaactacc gtgatgtctt ctctcccatc 321
 Ile

<210> 16
 <211> 97
 <212> PRT
 <213> Conus dalli

<400> 16
 Met Lys Leu Thr Cys Leu Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60

Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
 65 70 75 80

Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys
 85 90 95

Ile

<210> 17
 <211> 31
 <212> PRT
 <213> Conus dalli

<220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 4 and 29
 may be Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-

004493 004493

carboxy-Glu ; Xaa at residue 23 may be Trp or bromo-Trp;

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 17

Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe
1 5 10 15

Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Leu Leu Arg Xaa Cys Ile
20 25 30

<210> 18

<211> 321

<212> DNA

<213> Conus dalli

<220>

<221> CDS

<222> (1)..(291)

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1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

cag aga cgg gtc aag ccg tgc agt gaa gaa ggt caa ctt tgt gat cca 240
Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
65 70 75 80

ctt tct caa aac tgc tgc cgt ggc tgg cat tgc gtt ctt gtc tct tgc 288
Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys
85 90 95

gtc tgaaactacc gtgatgtctt ctctcccatc 321
Val

<210> 19

<211> 97

<212> PRT

<213> Conus dalli

<400> 19

Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

09749637.00100

Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
65 70 75 80

Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys
85 90 95

Val

<210> 20
<211> 30
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residues 6 and 7 may be Glu or gamma-carboxy-Glu ; Xaa at residue 22 may be Trp or bromo-Trp

<400> 20
Val Lys Xaa Cys Ser Xaa Xaa Gly Gln Leu Cys Asp Xaa Leu Ser Gln
1 5 10 15

Asn Cys Cys Arg Gly Xaa His Cys Val Leu Val Ser Cys Val
20 25 30

<210> 21
<211> 406
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (14)..(247)

<400> 21
aaacatcgcc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 49
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
1 5 10

ttc ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 97
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

ttg ggg aat ctt ttt tgg aat gca cat cac gaa atg aag aac ccc gaa 145
Leu Gly Asn Leu Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu
30 35 40

gcc tct aaa ttg aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt 193
Ala Ser Lys Leu Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys
45 50 55 60

aat ttg tta gac caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc 241
Asn Leu Leu Asp Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val
65 70 75

tgc aca taaaactgcc gtgatgtctt ctcttccct ctgtgctacc tggcttgatc 297

00445460

Cys Thr

tttgattggc gcgtgtcggt cactgggttat gaaccccccc cccccccccc cccccccct 357

tccggctctc tggaggcctc ggggggttcaa catccaaata aagtgcacag 406

<210> 22
 <211> 78
 <212> PRT
 <213> Conus textile

<400> 22
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

<210> 23
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 23
 Xaa Cys Lys Gln Asp Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

<210> 24
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
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 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 9 is Nle; Xaa at residue
 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
 yr or O-phospho-Tyr

<400> 24
 Xaa Cys Lys Gln Asp Gly Xaa Xaa Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

0974963-081304

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<210> 25
<211> 265
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(234)

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1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234
Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

taaaactgcc gtgatgtctt ctctctccct c 265

<210> 26
<211> 78
<212> PRT
<213> Conus magus

<400> 26
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

<210> 27
<211> 27
<212> PRT
<213> Conus magus

<220>
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<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 27

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<210> 28

<211> 27

<212> PRT

<213> Conus textile

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 28

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Phe Val Cys Thr
20 25

<210> 29

<211> 265

<212> DNA

<213> Conus distans

<220>

<221> CDS

<222> (1)..(234)

<400> 29

atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234
Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

taaaactgcc gtgatgtctt ctctccct c 265

<210> 30

<211> 78

T00T80"ZEGH460

<212> PRT
<213> Conus distans

<400> 30
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60
Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

<210> 31
<211> 27
<212> PRT
<213> Conus distans
<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 31
Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15
Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<210> 32
<211> 265
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (1)..(234)

<400> 32
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30
ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

caa aac tgc tgc gag ggc tat tgc ata gta ctt gtc tgc aca 234
 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

taaaactgcc gtgatgtctt ctctctcccct c 265

<210> 33
 <211> 78
 <212> PRT
 <213> Conus ammiralis

<400> 33
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

<210> 34
 <211> 27
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 7 and 1
 8 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr,
 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
 -Tyr

<400> 34
 Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
 1 5 10 15

Cys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

<210> 35
 <211> 256
 <212> DNA
 <213> Conus dalli

<220>
 <221> CDS
 <222> (1)..(225)

<400> 35
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30

<400> 38

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gcttgacagg tgaatttggc ttcacagttt tccactgtcg tctttggcat catctgaaac      60
atcgccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg      111
      Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
      1              5              10
acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg      159
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
15              20              25              30
aat att ttt tcg aat gca cat cac gaa atg aag aat ccc gaa gcc tct      207
Asn Ile Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser
      35              40              45
aaa ttg aac aag agg tgc cgt cta ggg gct gaa agt tgt gat gta att      255
Lys Leu Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile
      50              55              60
tca caa aac tgc tgc caa ggc acg tgc gtt ttt ttc tgc tta cca      300
Ser Gln Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro
      65              70              75
tgatgtcttc tattctcttc tgtgctacct ggcttgatct ttcattagcg cgtgcctttc      360
actgggttatg aacccccctga tccgactctc tggcagcctc ggggggttcaa catccaaata      420
aaacgacagc acaatgacaa a      441

<210> 39
<211> 77
<212> PRT
<213> Conus gloriamaris

<400> 39
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1              5              10              15
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Ile
      20              25              30
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
      35              40              45
Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile Ser Gln
      50              55              60
Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro
      65              70              75

<210> 40
<211> 26
<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
      26 may be Pro or hydroxy-Pro

<400> 40
Cys Arg Leu Gly Ala Xaa Ser Cys Asp Val Ile Ser Gln Asn Cys Cys
1              5              10              15

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<400>	42														
Met	Lys	Leu	Thr	Cys	Met	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala
1				5					10					15	
Trp	Thr	Phe	Ala	Thr	Ala	Asp	Asp	Pro	Arg	Asn	Gly	Leu	Glu	Lys	Leu
			20					25					30		
Phe	Ser	Asn	Thr	His	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Leu
		35					40					45			
Asn	Lys	Arg	Cys	Lys	Gln	Ala	Asp	Glu	Ser	Cys	Asn	Val	Phe	Ser	Leu
	50					55					60				
Asp	Cys	Cys	Thr	Gly	Leu	Cys	Leu	Gly	Phe	Cys	Val	Ser			
65					70					75					

<210> 43
 <211> 26
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

<400> 43
 Cys Lys Gln Ala Asp Xaa Ser Cys Asn Val Phe Ser Leu Asp Cys Cys
 1 5 10 15
 Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
 20 25

<210> 44
 <211> 242
 <212> DNA
 <213> Conus gloriamaris

<220>
 <221> CDS
 <222> (1)..(225)

<400> 44
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 tgg aca ttc gcc acg gcc atc acc agg aat gga ttg ggg aat ctt ttt 96
 Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
 20 25 30
 ccg aag aat cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg aac 144
 Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45
 aag agg tgc gtt cca tac gag gcc cct tgt aat tgg ctt aca caa aac 192
 Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
 50 55 60
 tgc tgc gat gag cta tgc gta ttt ttc tgc cta taaaactagc ctgatgt 242
 Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
 65 70 75

<210> 45
 <211> 75
 <212> PRT
 <213> Conus gloriamaris

<400> 45
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
 20 25 30
 Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45
 Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
 50 55 60

Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
65 70 75

<210> 46
<211> 25
<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 2 and 7 may be Pro or hydroxy-Pro; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-carboxy-Glu ; Xaa at residue 10 may be Trp or bromo-Trp

<400> 46
Cys Val Xaa Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
1 5 10 15

Asp Xaa Leu Cys Val Phe Phe Cys Leu
20 25

<210> 47
<211> 250
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(231)

<400> 47
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctc ttc ttg acc gtc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val
1 5 10 15

tgg aca ttc gcc acg gct gat gac tcc gga aat gga ttg gag aaa ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

ttt tgc aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc aaa caa gct gat gaa cct tgt gat gta ttt tca ctt 192
Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
50 55 60

gaa tgc tgc acc ggc ata tgt ctt gga ttc tgc acg tgg tgatgtcttc 241
Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

cctccccctc 250

<210> 48
<211> 77
<212> PRT
<213> Conus magus

<400> 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
50 55 60

Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

<210> 49
<211> 26
<212> PRT
<213> Conus magus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 7 may be Pro or hydroxy-Pro; Xaa at residue 26 may be Trp o
r bromo-Trp

<400> 49
Cys Lys Gln Ala Asp Xaa Xaa Cys Asp Val Phe Ser Leu Xaa Cys Cys
1 5 10 15

Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa
20 25

<210> 50
<211> 434
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (71)..(295)

<400> 50
gccttgacag gtgaatttgg cttcatagtt ttccactgtc gtctttggca tcatccaaaa 60

catcaccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
1 5 10

ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc agc aat gga ttg 157
Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu
15 20 25

gag aat ctt ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct 205
Glu Asn Leu Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser
30 35 40 45

aag ttg aac gag agg tgc ctt gat gct ggt gaa gtt tgt gat att ttt 253
Lys Leu Asn Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe
50 55 60

ttt cca aca tgc tgc ggc tat tgc att ctt ctt ttc tgc gca 295
Phe Pro Thr Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
65 70 75

taaaactacc gtgatgtctt ctactccct ctgtgctacc tggcttgatc tttgattggc 355

0974967-084304

gcgtaccctt cactggttat gaaaccctg atccagctct ctggaggcct cgggggttca 415
 acatccaaat aaagcgaca 434

<210> 51
 <211> 75
 <212> PRT
 <213> Conus textile

<400> 51
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45
 Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe Phe Pro Thr
 50 55 60
 Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
 65 70 75

<210> 52
 <211> 25
 <212> PRT
 <213> Conus textile

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-
 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

<400> 52
 Cys Leu Asp Ala Gly Xaa Val Cys Asp Ile Phe Phe Xaa Thr Cys Cys
 1 5 10 15
 Gly Xaa Cys Ile Leu Leu Phe Cys Ala
 20 25

<210> 53
 <211> 26
 <212> PRT
 <213> Conus textile

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidue 7 may be Pro or hydroxy-Pro

<400> 53
 Cys Ile Xaa Gln Phe Asp Xaa Cys Xaa Met Ile Arg His Thr Cys Cys
 1 5 10 15
 Val Gly Val Cys Phe Leu Met Ala Cys Ile
 20 25

<210> 54
 <211> 26

Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

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<400> 59
Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1      5      10      15
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Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
 35 40 45
 Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
 50 55 60
 Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 65 70 75

<210> 60
 <211> 26
 <212> PRT
 <213> Conus omaria

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

<400> 60
 Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
 1 5 10 15

Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 20 25

<210> 61
 <211> 259
 <212> DNA
 <213> Conus omaria

<220>
 <221> CDS
 <222> (1)..(228)

<400> 61
 atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
 20 25 30
 tta tca aat gca cat aac gaa atg aag aac ccc gaa gcc tct aca ttg 144
 Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu
 35 40 45
 aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt ata ctt tat tca 192
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
 50 55 60
 gac tgc tgc ggc tat tgc gtt ggt gct atc tgc cta taaaactacc 238
 Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu
 65 70 75
 gtgatgtctt ctctctccct c 259

<210> 62
 <211> 76
 <212> PRT

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<400>	64																
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Met	Lys	Leu	Thr	Cys	Val	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala		
1				5					10					15			
tgg	aca	ttc	gcc	acg	gct	gat	gac	ccc	aga	aat	gga	ttg	gag	aat	ctt	96	
Trp	Thr	Phe	Ala	Thr	Ala	Asp	Asp	Pro	Arg	Asn	Gly	Leu	Glu	Asn	Leu		
			20					25					30				
ttt	tcg	aag	aca	caa	cac	aaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	ttg	144	
Phe	Ser	Lys	Thr	Gln	His	Lys	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Leu		
		35					40					45					
aac	aag	agg	tgc	aaa	gca	gaa	aat	gaa	ctt	tgt	aat	ata	ttt	ata	caa	192	
Asn	Lys	Arg	Cys	Lys	Ala	Glu	Asn	Glu	Leu	Cys	Asn	Ile	Phe	Ile	Gln		
	50					55					60						
aac	tgc	tgc	gac	ggg	acg	tgc	ctt	ctt	atc	tgc	ata	caa	aat	cca	cag	240	

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

tgatgtcttc tctcctaccc tc

262

<210> 65
<211> 80
<212> PRT
<213> Conus aulicus

<400> 65
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
50 55 60

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

<210> 66
<211> 29
<212> PRT
<213> Conus aulicus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 4 and 6 may be Glu or gamma-carboxy-Glu; Xaa at re
sidue 28 may be Pro or hydroxy-Pro

<400> 66
Cys Lys Ala Xaa Asn Xaa Leu Cys Asn Ile Phe Ile Gln Asn Cys Cys
1 5 10 15

Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Xaa Gln
20 25

<210> 67
<211> 258
<212> DNA
<213> Conus aulicus

<220>
<221> CDS
<222> (1)..(228)

<400> 67
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gat aat cgt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
20 25 30

ttt tcg aag gca cgt cac gaa atg aat aac cgc aga gcc tct aaa ttg 144
Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu

097493700" 25954260

35 40 45
 aac aag agg tgc ctt gag ttt ggt gaa ctt tgt aat ttt ttt ttc cca 192
 Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
 50 55 60

acc tgc tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaactaccg 238
 Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 65 70 75

tgatgtcttc tcttccccctc 258

<210> 68
 <211> 76
 <212> PRT
 <213> Conus aulicus

<400> 68
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
 20 25 30

Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
 50 55 60

Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 65 70 75

<210> 69
 <211> 25
 <212> PRT
 <213> Conus aulicus

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
 o-Tyr

<400> 69
 Cys Leu Xaa Phe Gly Xaa Leu Cys Asn Phe Phe Phe Xaa Thr Cys Cys
 1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu
 20 25

<210> 70
 <211> 263
 <212> DNA
 <213> Conus dalli

<220>
 <221> CDS
 <222> (1)..(231)

<400> 70
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48

<210>	73
<211>	259
<212>	DNA
<213>	Conus distans

<220>
 <221> CDS
 <222> (1)..(228)

<400> 73
 atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg agg aat ctt 96
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
 20 25 30
 tta tcg aat gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca 192
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
 50 55 60
 gac tgc tgc agc tat tgc gtt ggt gct gtc tgc cta taaaactacc 238
 Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
 65 70 75
 gtgatgtctt ctactcccat c 259

<210> 74
 <211> 76
 <212> PRT
 <213> Conus distans

<400> 74
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
 20 25 30
 Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
 50 55 60
 Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
 65 70 75

<210> 75
 <211> 25
 <212> PRT
 <213> Conus distans

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues
 12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
 ulpho-Tyr or O-phospho-Tyr

<400> 75
 Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys
 1 5 10 15

0949637.081301

Ser Xaa Cys Val Gly Ala Val Cys Leu
20 25

<210> 76
<211> 262
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(231)

<400> 76
atg aaa ctg acg tgc ctg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gaa gac ccc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

ttt tcg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

gac aag agg tgc gtt aaa tat ctt gac cct tgt gac atg tta cgc cac 192
Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His
50 55 60

acc tgc tgc ttt ggc ctg tgc gta cta ata gcc tgc atc taaaactgcc 241
Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
65 70 75

gtgatgtctt ctactcccat c 262

<210> 77
<211> 77
<212> PRT
<213> Conus pennaceus

<400> 77
Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His
50 55 60

Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
65 70 75

<210> 78
<211> 26
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(26)

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<223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro

<400> 78

Cys Val Lys Xaa Leu Asp Xaa Cys Asp Met Leu Arg His Thr Cys Cys
1 5 10 15

Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
20 25

<210> 79

<211> 259

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (1)..(228)

<400> 79

atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gct tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac gag agg tgc ctt ggg ttt ggt gaa gtt tgc aat ttc ttt ttt cca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta taaaactacc 238
Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

gtgatgtctt ctattccoct c 259

<210> 80

<211> 76

<212> PRT

<213> Conus pennaceus

<400> 80

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

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<400>      83
Met  Lys  Leu  Thr  Cys  Val  Met  Leu  Val  Ala  Val  Leu  Phe  Leu  Thr  Ala
 1              5              10              15

Trp  Thr  Phe  Ala  Thr  Ala  Asp  Asp  Ser  Ser  Asn  Gly  Leu  Glu  Asn  Leu
      20              25              30

Phe  Ser  Lys  Ala  His  His  Glu  Met  Lys  Asn  Pro  Glu  Ala  Ser  Lys  Leu

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35 40 45
 Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His
 50 55 60
 Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
 65 70 75 80

<210> 84
 <211> 29
 <212> PRT
 <213> Conus pennaceus
 <220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro.

<400> 84
 Cys Ile Xaa Gln Phe Asp Xaa Cys Asp Met Val Arg His Thr Cys Cys
 1 5 10 15
 Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
 20 25

<210> 85
 <211> 260
 <212> DNA
 <213> Conus pennaceus
 <220>
 <221> CDS
 <222> (1)..(240)

<400> 85
 atg aaa ctg acg tgc ttg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ttt 96
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
 20 25 30
 ttt tgc aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag agg tgc aaa gca gaa agt gaa gct tgt aat ata att aca caa 192
 Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln
 50 55 60
 aac tgc tgc gac ggc aag tgc ctt ttt ttc tgc ata caa att cca gag 240
 Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu
 65 70 75 80
 tgatgtcttc tcctcccatc 260

<210> 86
 <211> 80
 <212> PRT
 <213> Conus pennaceus

<400> 86
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala

094963 084300

1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
20 25 30

Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln
50 55 60

Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu
65 70 75 80

<210> 87
<211> 29
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 4, 6 and 29 may be Glu or gamma-carboxy-Glu; Xaa
at residue 28 may be Pro or hydroxy-Pro

<400> 87
Cys Lys Ala Xaa Ser Xaa Ala Cys Asn Ile Ile Thr Gln Asn Cys Cys
1 5 10 15

Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Xaa Xaa
20 25

<210> 88
<211> 632
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (110)..(199)

<400> 88
ggtcgacatc atcatcatca tcgatccatc tgtccatcca tccattcatt cattcgctgc 60
cagactgtca taaatattcg agtctctcct tctgtttgta tctgacaga ttg aac aag 118
Leu Asn Lys
1

agg tgc att gac ggt ggt gaa att tgt gat att ttt ttt cca aac tgc 166
Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe Pro Asn Cys
5 10 15

tgc agt ggg tgg tgc att att ctc gtc tgc gca tgaaactacc gtgatgtctt 219
Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala
20 25 30

ctactcccct ctagtagtag tagggggcgc ctctagagga tocaagctta cgtacgcgtg 279
catgcgacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 339
acaacgtcgt gactgggaaa accctggcgt taccacaactt aatgcgcttg cagcacatcc 399
cccttttcgcc agctggcgta atagcgaaga ggcccgcacc gatcgccctt ccaacagttt 459

ggcgcagcctg aatggcgaat gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt 519
 ggtgggtacg cgcagcgtga ccggtacact tgccagcgcc ctagcgcccg ctccttttgc 579
 tttcttcctt tcctttctcg ccaccgttcg cccgggggtt tcccgtcaag etc 632

<210> 89
 <211> 30
 <212> PRT
 <213> Conus omaria

<400> 89
 Leu Asn Lys Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe
 1 5 10 15
 Pro Asn Cys Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala
 20 25 30

<210> 90
 <211> 26
 <212> PRT
 <213> Conus omaria
 <220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 mo-Trp

<400> 90
 Cys Ile Asp Gly Gly Xaa Ile Cys Asp Ile Phe Phe Xaa Asn Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys Ile Ile Leu Val Cys Ala
 20 25

<210> 91
 <211> 650
 <212> DNA
 <213> Conus omaria

<220>
 <221> CDS
 <222> (107)..(196)

<400> 91
 ggtcgacatc atcatcatcg atccatctgt ccattccatcc attcattcat tcgctgccag 60
 actgtcataa atattcgagt ctctccttct gtttgtatct gacaga ttg aac aag .115
 Leu Asn Lys
 1

agg tgc ctt gac ggt ggt gaa att tgt ggt att ttg ttt cca agc tgc 163
 Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro Ser Cys
 5 10 15

tgc agt ggg tgg tgc att gtt ctc gtc tgc gca tgaaactacc gtgatgtctt 216
 Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 20 25 30

ctactcccct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 276
 catgcgacgt catagctctt ctatagtgtc acctaaattc aattcaactgg ccgtcgtttt 336

09749637.081304

acaacgtcgt gactgggaaa accctggcgt tacccaactt aatcgcccttg cagcacatcc 396
 cccttttcgcc agctggcgta atagcgaaga ggcccgcacc gatcgccctt cccaacaagt 456
 tgcgcagcct gaatggcgaa tgggacgcgc cctgtagcgg cgcattaagc ggggcgggtg 516
 tgggtggttac ggcgaccgtg accgctacac ttgccagcgc cctagccgcc cgctcctttc 576
 gctttctttcc ctctctttct cgcacgttcg gccggctttc cccgtcaagc tctaaatcgg 636
 gggcttcctt tttta 650

<210> 92
 <211> 30
 <212> PRT
 <213> Conus omaria

<400> 92
 Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe
 1 5 10 15
 Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 20 25 30

<210> 93
 <211> 26
 <212> PRT
 <213> Conus omaria

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 mo-Trp

<400> 93
 Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
 20 25

<210> 94
 <211> 618
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (107)..(193)

<400> 94
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 actgtaataa atattcgagt ctctctttct gtttgatatc gacaga ttg aac aag 115
 Leu Asn Lys
 1
 agg tgc ctt gag ttt ggt gaa gtt tgt aat ttt ttt ttc cca acc tgc 163
 Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe Pro Thr Cys
 5 10 15
 tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaaactacc gtgatgtctt 213

Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25

ctactccoct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgctg 273
catgcgacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 333
acaacgtcgt gactgggaaa accctggcgt tacccaactt aatcgccctg cagcacatcc 393
ccctttcgcc agctggcgta atagcgaaga ggcccgacc gatcgccctt cccaacagtt 453
gcgagcctg aatggcgaat gggacgcgcc ctgtagcggc gcattaagcg cggcggtgt 513
ggtggttacg cgcagcgtga ccgctacact tgcagcgccc tagcgcccg ccttttcgct 573
tttttccctt cctttctcgc cagtttcgcc ggctttcccc gtcaa 618

<210> 95
<211> 29
<212> PRT
<213> Conus marmoreus

<400> 95
Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
1 5 10 15

Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25

<210> 96
<211> 25
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
o-Tyr

<400> 96
Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu
20 25

<210> 97
<211> 444
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (150)..(236)

<400> 97
gaaagctggt acgcctgcag gtaccgggcc ggaattcccg ggtcgacatc atcatcatca 60
tcgatccatc tgtccatcca tccattcatt cattcgctgc cagactgtaa taaatattcg 120
agttttctct tctgtttgta tctgacagg ttg aac aag agg tgc caa gag ttc 173

Leu Asn Lys Arg Cys Gln Glu Phe
1 5

ggt gaa gtt tgt aat ttt ttt ttc cca gac tgc tgc ggc tat tgc gtt 221
Gly Glu Val Cys Asn Phe Phe Phe Pro Asp Cys Cys Gly Tyr Cys Val
10 15 20

ctt tta ctc tgc ata taaaactacc gtgatgtctt ctcttcccat ctagtagtag 276
Leu Leu Leu Cys Ile
25

tagtagtagt aggcggccgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc 336

atagctcttc tatagtgtca cctaaattca attcactggc cgtcgtttta caaccgtcgt 396

gactgggaaa accctggcgt tcccaactta attcgccttg cagcacat 444

<210> 98
<211> 29
<212> PRT
<213> Conus marmoreus

<400> 98
Leu Asn Lys Arg Cys Gln Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
1 5 10 15

Pro Asp Cys Cys Gly Tyr Cys Val Leu Leu Leu Cys Ile
20 25

<210> 99
<211> 25
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr,
125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
-Tyr

<400> 99
Cys Gln Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asp Cys Cys
1 5 10 15

Gly Xaa Cys Val Leu Leu Leu Cys Ile
20 25

<210> 100
<211> 545
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (153)..(242)

<220>
<221> misc_feature
<222> (1)..(545)
<223> n may be any nucleotide

<400> 100

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ttttgaagcn ggtagcgctg cagggtaccgg tccggaattc ccgggtcgac atcatcatca      60
tcatcgatcc atctgtccat ccattccattc attcattogc taccagactg taataaatat      120
tcgggtctct ctttctgttt gtatctgaca ga ttg gac aag agg tgc att cca      173
                                Leu Asp Lys Arg Cys Ile Pro
                                1                    5

cat ttt gac cct tgt gac ccg ata cgc cac acc tgc tgc ttt ggc ctg      221
His Phe Asp Pro Cys Asp Pro Ile Arg His Thr Cys Cys Phe Gly Leu
      10                    15                    20

tgc cta cta ata gcc tgc atc taaaactgcc gtgatgtctt ctctcccct      272
Cys Leu Leu Ile Ala Cys Ile
      25                    30

ctagtagtag taggcggcgc ctctagagga tccaagctta cgtacgcgtg catgcgacgt      332
catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt acaacgtogt      392
gactgggaaa accctggcgt tacccaactt aatcgcccttg cagcacatcc ccctttcgcc      452
agctggcgta atagcgaaga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg      512
aatggcgaat gggacgcgcc ctgtagcggc gct      545

<210> 101
<211> 30
<212> PRT
<213> Conus omaria

<400> 101
Leu Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg
1          5          10          15

His Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
      20          25          30

<210> 102
<211> 26
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

<400> 102
Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
1          5          10          15

Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
      20          25

<210> 103
<211> 534
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (140)..(226)

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<400> 103
 ggtaacgctg caggtaccgg tccggaattc ccgggtcgac atcatcatca tccatccatc 60
 tgtccatcca tccattcttt catttgctgc cagactgtaa taaatattcg agtctctctt 120
 tctgtttgta tctgacaga ttg aac aag agg tgc ctt gag ttt ggt gaa gtt 172
 Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val
 1 5 10
 tgt aat ttt ttt ttc cca acc tgc tgc ggc tat tgc gtt ctt ctt gtc 220
 Cys Asn Phe Phe Phe Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val
 15 20 25
 tgc cta taaaactacc gtgatgtctt ctcttccoct ctagtagtag taggcggccg 276
 Cys Leu

ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc 336
 acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt 396
 tacccaactt aatcgcttg cagcacatcc ccttttcgcc agctggcgta atagcgaaga 456
 ggcccgacc gatcgccctt cccaacagtt ggcgcgctg aatggcgaat gggacgcgcc 516
 ctgtagcggc gcattaag 534

<210> 104
 <211> 29
 <212> PRT
 <213> Conus omaria

<400> 104
 Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
 1 5 10 15
 Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 20 25

<210> 105
 <211> 25
 <212> PRT
 <213> Conus omaria

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidue13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
 o-Tyr

<400> 105
 Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
 1 5 10 15
 Gly Xaa Cys Val Leu Leu Val Cys Leu
 20 25

<210> 106
 <211> 200
 <212> DNA
 <213> Conus obscurus

094963 0304

<220>
 <221> CDS
 <222> (73)..(180)

<400> 106
 cgatccatct gtccatccat ccattcgttc gtccgctgcc aaactgtaat aaataaccga 60

gtctctctgt tt gta tct gac aga tcg aaa aag caa tgc cgt caa aat ggt 111
 Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly
 1 5 10

gaa gtg tgt gat gcg aat ttg gca cac tgc tgc agt ggc ccg tgt ttt 159
 Glu Val Cys Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe
 15 20 25

ctc ttc tgt cta aac cag ccg tgatgtcttc tactccctc 200
 Leu Phe Cys Leu Asn Gln Pro
 30 35

<210> 107
 <211> 36
 <212> PRT
 <213> Conus obscurus

<400> 107
 Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly Glu Val Cys
 1 5 10 15

Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe Leu Phe Cys
 20 25 30

Leu Asn Gln Pro
 35

<210> 108
 <211> 32
 <212> PRT
 <213> Conus obscurus

<220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residue 10 may be Glu or gamma-carboxy-Glu; Xaa at residue
 s 23 and 32 may be Pro or hydroxy-Pro

<400> 108
 Ser Lys Lys Gln Cys Arg Gln Asn Gly Xaa Val Cys Asp Ala Asn Leu
 1 5 10 15

Ala His Cys Cys Ser Gly Xaa Cys Phe Leu Phe Cys Leu Asn Gln Xaa
 20 25 30

<210> 109
 <211> 262
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (1)..(231)

<400> 109
 atg aaa ctg acg tgc gtg atg atc att gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala

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1          5          10          15
tgg aca ttt gcc acg gct gat gac tcc gga aat gga ttg gaa aat ctt          96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
                20                25                30

ttt tcg aag gca cat cac gaa atg aag aac ccc aaa gcc tct aaa ttg          144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
                35                40                45

aac aag agg tgc act caa agc ggt gaa ctt tgt gat gtg ata gac cca          192
Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
                50                55                60

gac tgc tgc aat aat ttt tgc att ata ttt ttc tgc ata taaaactgcc          241
Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
        65                70                75

gtgatgtctt ctactcccct c          262

<210> 110
<211> 77
<212> PRT
<213> Conus ammiralis

<400> 110
Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala
1          5          10          15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
                20                25                30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
                35                40                45

Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
                50                55                60

Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
        65                70                75

<210> 111
<211> 26
<212> PRT
<213> Conus ammiralis

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
        13 may be Pro or hydroxy-Pro

<400> 111
Cys Thr Gln Ser Gly Xaa Leu Cys Asp Val Ile Asp Xaa Asp Cys Cys
1          5          10          15

Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
                20                25

<210> 112
<211> 286
<212> DNA
<213> Conus textile

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<222> (25) .. (255)

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ggcattacct aaaacatcac caaa atg aaa ctg acg tgc atg atg atc gtt      51
                        Met Lys Leu Thr Cys Met Met Ile Val
                        1           5

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gct gtg ctg ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc 99
Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser
10 15 20 25

gga aat gga ttg gag aaa ctt ttt tcg aat gca cat cac gaa atg aag 147
Gly Asn Gly Leu Glu Lys Leu Phe Ser Asn Ala His His Glu Met Lys
30 35 40

aac ccc gaa gcc tct aat ttg aac aag agg tgc gct cct ttt ctt cac 195
Asn Pro Glu Ala Ser Asn Leu Asn Lys Arg Cys Ala Pro Phe Leu His
45 50 55

ctt tgt acc ttt ttc ttc cca aac tgc tgc aac ggc tat tgc gtt caa 243
Leu Cys Thr Phe Phe Phe Pro Asn Cys Cys Asn Gly Tyr Cys Val Gln
60 65 70

ttt atc tgc cta taaaactact gtgatgtctt ctattcccct c 286
Phe Ile Cys Leu
75

<213> Conus textile

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Asn Leu
35 40 45

Asn Lys Arg Cys Ala Pro Phe Leu His Leu Cys Thr Phe Phe Phe Pro
50 55 60

Asn Cys Cys Asn Gly Tyr Cys Val Gln Phe Ile Cys Leu
65 70 75

<213> Conus textile

<223> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

Cys Ala Xaa Phe Leu His Leu Cys Thr Phe Phe Phe Xaa Asn Cys Cys

1 5 10 15

Asn Gly Xaa Cys Val Gln Phe Ile Cys Leu
20 25

<210> 115
<211> 484
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (74)..(304)

<400> 115
ggatcctagc acagtgaatt tggcttcaca gttttccact gtcgtctttg gcacatcca 60

aaacatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
1 5 10

ttc ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

ttg gag aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc aaa 205
Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys
30 35 40

gac tct aaa ttg aac aag agg tgc ctt gac gct ggt gaa atg tgt gat 253
Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp
45 50 55 60

ctt ttt aat tca aaa tgc tgc agt ggg tgg tgc att att ctc ttc tgc 301
Leu Phe Asn Ser Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys
65 70 75

gca taaaactacc gtgatgtctt ctactcccct ctgtgctacc tggcttgatc 354
Ala

tttgattggc gcgtgccctt cactgggttat gaacccccct gatccgactc tctggcggcc 414

tgcgggggttc aacatccaaa taaagccgac acgatactga cgtagaaaaa aaaaaaaaaa 474

aaaaaaaaaa 484

<210> 116
<211> 77
<212> PRT
<213> Conus marmoreus

<400> 116
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp Leu Phe Asn Ser
50 55 60

<210>	119
<211>	77
<212>	PRT

<213> Conus marmoreus

<400> 119

Met Lys Leu Thr Ser Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro
50 55 60

Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
65 70 75

<210> 120

<211> 26

<212> PRT

<213> Conus marmoreus

<220>

<221> SITE

<222> (1)..(26)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
mo-Trp

<400> 120

Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
20 25

<210> 121

<211> 470

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (70)..(303)

<400> 121

gctagcacag tgaatttggc ttcacagttt tccactgtcg tctttggcat catccaaaac 60

atcaccaag atg aaa ctg acg tgc atg atg atc gaa gca gag ctg ttc ttg 111
Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag 159
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
15 20 25 30

aat ctt ttt tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct 207
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt 255
Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
50 55 60

0974963.001

gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cct ata 303
 Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
 65 70 75

taactaccgt gatgtcttct actccctct gtgctgcctg gcttgatctt tgattggcgc 363

gtgcccttca ctgggttatga accccctga tccgactctc ttgcggcctc aggggttcaa 423

catccaaata aagcgacacg aaaatgaaaa aaaaaaaaaa aaaaaaa 470

<210> 122

<211> 78

<212> PRT

<213> Conus marmoreus

<400> 122

Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
 65 70 75

<210> 123

<211> 27

<212> PRT

<213> Conus marmoreus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residues 2 and 26 may be Pro or hydroxy-Pro; Xaa at residues 6 and 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 123

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
 1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Xaa Ile
 20 25

<210> 124

<211> 470

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (67)..(312)

<400> 124

ttgcacggtg aatttcgctt atatttttct actgtcgtct ttggcatcat ccaaaacatc 60

accaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 108

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta ttg 156
Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu
15 20 25 30

gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc 204
Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala
35 40 45

tct aaa ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt 252
Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe
50 55 60

tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc 300
Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe
65 70 75

ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattcccct ctgtgctacc 352
Leu Trp Cys Ala
80

tggtttgatc tttgattggc gcgtgccctt cagtgggttat gaacccccct gatccgactc 412

tctggggggcc tcggggggttc aacatccaaa taaagctgac aacacaataa aaaaaaaaa 470

<210> 125
<211> 82
<212> PRT
<213> Conus marmoreus

<400> 125
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
65 70 75 80

Cys Ala

<210> 126
<211> 30
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
s 24 and 28 may be Trp or bromo-Trp

<400> 126
Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile

1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 127
<211> 277
<212> DNA
<213> Conus striatus

<220>
<221> CDS
<222> (1)..(246)

<400> 127
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gca ttg gag aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn
20 25 30

ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc tct aaa 144
Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
35 40 45

ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt tgt ggc 192
Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
50 55 60

ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc ctc tgg 240
Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
65 70 75 80

tgc gca taaaactgcc gtgatgtctt ctccctccct c 277
Cys Ala

<210> 128
<211> 82
<212> PRT
<213> Conus striatus

<400> 128
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
65 70 75 80

Cys Ala

<210> 129
<211> 30
<212> PRT

09749637.08.30.1

<213> Conus striatus

<220>

<221> SITE

<222> (1)..(30)

<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp

<400> 129

Asp Asp Xaa Cys Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 130

<211> 277

<212> DNA

<213> Conus omaria

<220>

<221> CDS

<222> (1)..(246)

<400> 130

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gaa aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

ctt tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

ttg aac acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc 192
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

atg ata aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

tgc gcc taaaactgcc gtgatgtctt ctccctccct c 277
Cys Ala

<210> 131

<211> 82

<212> PRT

<213> Conus omaria

<400> 131

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

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Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

Cys Ala

<210> 132

<211> 30

<212> PRT

<213> Conus omaria

<220>

<221> SITE

<222> (1)..(30)

<223> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
be Trp or bromo-Trp

<400> 132

Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

<210> 133

<211> 277

<212> DNA

<213> Conus aulicus

<220>

<221> CDS

<222> (1)..(246)

<400> 133

atg aaa ctg acg tgc ctg atg ata gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gag aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

ctt tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

ttg aac acg aga gac tac gat tgc gaa cct cct gga aat ttt tgt ggc 192
Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

atg ata aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

tgc gcc taaaactgcc gtgatgtctt ctctccct c 277
Cys Ala

<210> 134

<211> 82

<212> PRT

<213> Conus aulicus

09749637.081304

<400> 134
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30
 Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
 35 40 45
 Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
 50 55 60
 Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
 65 70 75 80

Cys Ala

<210> 135
 <211> 30
 <212> PRT
 <213> Conus aulicus
 <220>
 <221> SITE
 <222> (1)..(30)
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or
 gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or
 hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 135
 Asp Xaa Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
 1 5 10 15
 Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
 20 25 30

<210> 136
 <211> 685
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (111)..(212)

<400> 136
 ggtcgacatc atcatcatca tcgatccatc tgtccatcca tctattcatt cattcgtggc 60
 caaactgtaa taaataatgc aagtctctct ttctgtttgt atctgacaga ttg aac 116
 Leu Asn
 1
 acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc atg ata 164
 Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile
 5 10 15
 aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc tgc gcc 212
 Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala
 20 25 30
 taaaactgcc gtgatgtctt ctcttccct ctagtagtag taggcggccg ctctagagga 272

00749537.034304

tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc acctaaattc 332
aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt tacccaactt 392
aatcgccttg cagcacatcc ccctttcgcg agctggcgta atagcgaaga ggcccgaccc 452
gatcgccott cccaacagtt gcgcagcctg aatggcgaat gggacgcgcc ctgtagcggc 512
gcattaagcg cggcgggtgt ggtggttacg ccgcagccgt gacccgctac acttgccagc 572
gccctagcgc ccgctccttt cgtttcttct cttcctttct cgcacgcttc gccggctttt 632
cccgtaagc tctaaatcgg gggtccttt aggtccgat ttaagtgtt tac 685

<210> 137
<211> 34
<212> PRT
<213> Conus marmoreus

<400> 137
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
1 5 10 15
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
20 25 30

Cys Ala

<210> 138
<211> 30
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
be Trp or bromo-Trp

<400> 138
Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15
Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

<210> 139
<211> 126
<212> DNA
<213> Conus regius

<220>
<221> CDS
<222> (1)..(96)

<400> 139
ttg aac cag aga gac tgc ctt agt aaa aac gct ttc tgt gcc tgg ccg 48
Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
1 5 10 15
ata ctt gga cca ctg tgc tgc agt ggc tgg tgc tta tac gtc tgc atg 96
Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
20 25 30

0974953-2E964260

taaaactgcc gtgatgtctt ctatccctc

126

<210> 140

<211> 32

<212> PRT

<213> Conus regius

<400> 140

Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
1 5 10 15

Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
20 25 30

<210> 141

<211> 28

<212> PRT

<213> Conus regius

<220>

<221> SITE

<222> (1)..(28)

<223> Xaa at residues 11 and 22 may be Trp or bromo-Trp; Xaa at residue
s 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be T
yr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
pho-Tyr

<400> 141

Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
1 5 10 15

Leu Cys Cys Ser Gly Xaa Cys Leu Xaa Val Cys Met
20 25

<210> 142

<211> 133

<212> DNA

<213> Conus radiatus

<220>

<221> CDS

<222> (2)..(103)

<400> 142

a ttg aac aag aaa ggt gat gac tgc ctt gct gtt aaa aaa aat tgt ggc 49
Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
1 5 10 15

ttt cca aaa ctt gga ggg cca tgc tgc agt ggc ttg tgc ttt ttc gtc 97
Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
20 25 30

tgc gcc taaaactgcc gtgatgtctt ctctccctt
Cys Ala

133

<210> 143

<211> 34

<212> PRT

<213> Conus radiatus

<400> 143

Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
1 5 10 15

09749637.084304

Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
 20 25 30

Cys Ala

<210> 144
 <211> 30
 <212> PRT
 <213> Conus radiatus

<220>
 <221> SITE
 <222> (1)..(30)
 <223> Xaa at residues 14 and 19 may be Pro or hydroxy-Pro.

<400> 144
 Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly Phe Xaa Lys Leu
 1 5 10 15

Gly Gly Xaa Cys Cys Ser Gly Leu Cys Phe Phe Val Cys Ala
 20 25 30

<210> 145
 <211> 127
 <212> DNA
 <213> Conus regius

<220>
 <221> CDS
 <222> (1)..(96)

<400> 145
 ttg aat cag agc gac tgc ctt cct aga gac aca ttc tgt gcc ttg ccg 48
 Leu Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
 1 5 10 15

caa ctt gga cta ctg tgc tgc agt ggc cgg tgc tta ctc ttc tgc gtg 96
 Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
 20 25 30

taaaactgcc gtgatgtctt ctctctccct c 127

<210> 146
 <211> 32
 <212> PRT
 <213> Conus regius

<400> 146
 Leu Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
 1 5 10 15

Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
 20 25 30

<210> 147
 <211> 28
 <212> PRT
 <213> Conus regius

<220>
 <221> SITE
 <222> (1)..(28)
 <223> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro.

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<211> 27

<212> PRT
<213> Conus aurisiacus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 150
Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr
20 25

<210> 151
<211> 412
<212> DNA
<213> Conus purpurascens

<220>
<221> CDS
<222> (1)..(243)

<400> 151
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

gac aaa aag gaa gcc tgc tat gcg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

ccc ggg cta tgc tgc agt gag ttt tgt ctc ccg ggc gtc tgc ttc ggt 240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
65 70 75 80

ggt taactgccgt gatgtcttct actccctct gtgctacctg gcttgatctt 293
Gly

tgatcggcgt gtgcccttca ctgggtatga acccactgat cttacctctc ttgaaggacc 353

tctgggggtcc agcatccaaa taagcgacat cccaatgaaa aaaaaaaaaa aaaaaaaaaa 412

<210> 152
<211> 81
<212> PRT
<213> Conus purpurascens

<400> 152
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

094937.081360

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45

Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
 65 70 75 80

Gly

<210> 153

<211> 29

<212> PRT

<213> Conus purpurascens

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
 o or hydroxy-Pro

<400> 153

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
 20 25

<210> 154

<211> 29

<212> PRT

<213> Conus purpurascens

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
 o or hydroxy-Pro

<400> 154

Xaa Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
 20 25

<210> 155

<211> 29

<212> PRT

<213> Conus purpurascens

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su

lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 155

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ala Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<210> 156

<211> 29

<212> PRT

<213> Conus purpurascens

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 156

Xaa Ala Cys Xaa Ala Xaa Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<210> 157

<211> 289

<212> DNA

<213> Conus magus

<220>

<221> CDS

<222> (1)..(252)

<400> 157

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt 192
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
50 55 60

cca gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt 240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

gtt gat tct ggc taacagtgtg cggttggttag tgtcttctcc tcccctc 289
Val Asp Ser Gly

<210> 158

<211> 84
 <212> PRT
 <213> Conus magus

<400> 158
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 Val Asp Ser Gly

<210> 159
 <211> 32
 <212> PRT
 <213> Conus magus

<220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
 hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
 Xaa at residue 25 may be Trp or bromo-Trp

<400> 159
 Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
 1 5 10 15
 Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser
 20 25 30

<210> 160
 <211> 273
 <212> DNA
 <213> Conus magus

<220>
 <221> CDS
 <222> (1)..(249)

<400> 160
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa 192
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60

cca gga ctt tgc tgc agc gcg ata tgc tta tgc ttt gtc tgc ata tca 240
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80

ttt gat ttt tgattgatgt cttctcctcc cctc 273
 Phe Asp Phe

<210> 161
 <211> 83
 <212> PRT
 <213> Conus magus

<400> 161
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80

Phe Asp Phe

<210> 162
 <211> 32
 <212> PRT
 <213> Conus magus

<220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residue 2 may be Glu or gamma-carboxy-Glu; Xaa at residue
 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr; Xaa at residues 5, 6 and 14 may be Pro or hydro
 xy-Pro

<400> 162
 Asp Xaa Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
 20 25 30

<210> 163
 <211> 289
 <212> DNA
 <213> Conus magus

<220>
 <221> CDS
 <222> (1)..(252)

00749637.003304

<400> 163
 atg aaa ctg acg tgc gtg atg atc gtt gct gta ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30

ttt ccg aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac cag aga gaa gcc tgc tat aat gct ggt tca ttt tgt ggc atc cat 192
 Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His
 50 55 60

cca gga ctc tgc tgc agc gag ttt tgc att ctt tgg tgc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe
 65 70 75 80

gtt gat tct ggc taactgtgtg cgttggttga tgtcttctcc tcccatc 289
 Val Asp Ser Gly

<210> 164
 <211> 84
 <212> PRT
 <213> Conus magus

<400> 164
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30

Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe
 65 70 75 80

Val Asp Ser Gly

<210> 165
 <211> 32
 <212> PRT
 <213> Conus magus

<220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydrox
 y-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 165
 Xaa Ala Cys Xaa Asn Ala Gly Ser Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15

<210>	168
<211>	32
<212>	PRT
<213>	Conus magus

<220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro

<400> 168
 Xaa Ala Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
 20 25 30

<210> 169
 <211> 272
 <212> DNA
 <213> Conus ermineus

<220>
 <221> CDS
 <222> (1)..(243)

<400> 169
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30
 ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45
 gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
 65 70 75 80
 ggt taactgccgt gatgtcttct cctcccctc 272
 Gly

<210> 170
 <211> 81
 <212> PRT
 <213> Conus ermineus

<400> 170
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60

Gly

 $\langle 211 \rangle$

<212> PRT

<213> Conus ermineus

 $\langle 220 \rangle$

<221> SITE

<222> (1) .. (29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be Pro or hydroxy-Pro

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

$\langle 211 \rangle$ 272

<212> DNA

<213> Conus purpurascens

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (243)$

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg	aca	ttc	gtc	acg	gct	gat	gac	tcc	aaa	aat	gga	ctg	gag	aat	cat		96
Trp	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Lys	Asn	Gly	Leu	Glu	Asn	His		
			20					25				30					

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

ggt taactgccgt gatgttttt cctccccctc 272
Gly

<211> 81

<212> PRT

<213> Conus purpurascens

<400> 173

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
 65 70 75 80

Gly

<210> 174
 <211> 29
 <212> PRT
 <213> Conus purpurascens
 <220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 14 and 24 may be Pro o
 r hydroxy-Pro

<400> 174
 Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15
 Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
 20 25

<210> 175
 <211> 266
 <212> DNA
 <213> Conus striatus

<220>
 <221> CDS
 <222> (1)..(246)

<400> 175
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc act 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga gaa ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
 Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
 50 55 60
 cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240

094937 081004

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

att gat tgatgtcttc tcctcccttc
Ile Asp

266

<210> 176
<211> 82
<212> PRT
<213> Conus striatus

<400> 176
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

Ile Asp

<210> 177
<211> 31
<212> PRT
<213> Conus striatus

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tr
p or bromo-Trp

<400> 177
Xaa Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
20 25 30

<210> 178
<211> 266
<212> DNA
<213> Conus striatus

<220>
<221> CDS
<222> (1)..(246)

<400> 178
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc act
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

48

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu

96

09457-08150

20										25										30										
ttt	ccg	aag	gca	cgt	cat	gaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	ttg		144													
Phe	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Leu															
		35					40					45																		
aac	aag	aga	gat	ggg	tgc	tct	agt	ggg	ggg	aca	ttt	tgt	ggc	atc	cat		192													
Asn	Lys	Arg	Asp	Gly	Cys	Ser	Ser	Gly	Gly	Thr	Phe	Cys	Gly	Ile	His															
	50					55					60																			
cca	gga	ctc	tgc	tgc	agc	gag	ttt	tgc	ttt	ctt	tgg	tgc	ata	aca	ttt		240													
Pro	Gly	Leu	Cys	Cys	Ser	Glu	Phe	Cys	Phe	Leu	Trp	Cys	Ile	Thr	Phe															
65					70					75					80															
att	gat	tgatgtcttc	tcctcccttc														266													
Ile	Asp																													

<210> 179
 <211> 82
 <212> PRT
 <213> Conus striatus

<400> 179
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

Ile Asp

<210> 180
 <211> 31
 <212> PRT
 <213> Conus striatus

<220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 180
Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15
Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
20 25 30

<210> 181
 <211> 31
 <212> PRT
 <213> Conus striolatus

<220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residues 6 and 14 may be Pro or hydroxy-Pro; Xaa at residue 31 may be Glu or gamma-carboxy-Glu

<400> 181
 Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15
 Cys Cys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
 20 25 30

<210> 182
 <211> 345
 <212> DNA
 <213> Conus catus

<220>
 <221> CDS
 <222> (1)..(234)

<400> 182
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60
 cca gga ctc tgc tgc agc gag ctt tgc ctg gtt tgg tgc aca 234
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
 65 70 75
 tgagtgtat tcttctggta cattttgtgg cttcaacgga ggactctgct gcagcaacct 294
 ttgcttattt tcgtgtgctt aacatttcgt gatgtcttct ctattcccct c 345

<210> 183
 <211> 78
 <212> PRT
 <213> Conus catus

<400> 183
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60

T03780-2E954250

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
 65 70 75

<210> 184
 <211> 27
 <212> PRT
 <213> Conus catus

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 184
 Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr
 20 25

<210> 185
 <211> 345
 <212> DNA
 <213> Conus catus

<220>
 <221> CDS
 <222> (1)..(234)

<400> . 185
 atg aaa ctg acg tgt atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60

cca gga ctc tgc tgc agc gag ctt tgc ctg ggt tgg tgc aca 234
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
 65 70 75

tgagtgttat tctactggta cattttgtgg cttcaacgga ggactctgct gcagcaacct 294

ttgcttattt tcgtgtgctt aacatttctg gatgtcttct ctattccct c 345

<210> 186
 <211> 78
 <212> PRT
 <213> Conus catus

<400> 186
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
65 70 75

<210> 187

<211> 27

<212> PRT

<213> Conus catus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 187

Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Gly Xaa Cys Thr
 20 25

<210> 188

<211> 266

<212> DNA

<213> Conus distans

<220>

<221> CDS

<222> (1)..(246)

<400> 188

atg aaa ctg acg tgt ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctc 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30

tct ccg aag gca cct cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
 35 40 45

aac aag aga tat gag tgc tat cta ctg gta cat ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
50 55 60

gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

266

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<210> 189
<211> 82
<212> PRT
<213> Conus distans
```

<400> 189

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

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<210> 190
<211> 31
<212> PRT
<213> Conus distans
```

 $\langle 220 \rangle$

<221> SITE

<222> (1) .. (31)

<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

$\langle 400 \rangle$ 190

Xaa Xaa Cys Xaa Leu Leu Val His Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<210>	191
<211>	113
<212>	DNA
<213>	Conus regius

 $\langle 220 \rangle$

<221> CDS

<222> (1) .. (93)

<400> 191

ttg	agc	aag	aga	gac	tgc	ctt	cct	gac	tac	acg	att	tgt	gcc	ttc	aat	48
Leu	Ser	Lys	Arg	Asp	Cys	Leu	Pro	Asp	Tyr	Thr	Ile	Cys	Ala	Phe	Asn	
1				5					10					15		

atg ggt ctg tgc tgc agc gac aag tgc atg ctc gtc tgc ctg ccg 93
Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro
20 25 30

tgatgtcttc tcctccctc 113

<211> 28
 <212> PRT
 <213> Conus regius

<220>
 <221> SITE
 <222> (1)..(28)
 <223> Xaa at residues 5 and 28 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 196
 Ile Ile Cys Gly Xaa Asp Xaa Met Phe Cys Gly Val Asn Val Phe Leu
 1 5 10 15
 Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Xaa
 20 25

<210> 197
 <211> 259
 <212> DNA
 <213> Conus gloriamaris

<220>
 <221> CDS
 <222> (1)..(228)

<400> 197
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gcg ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30
 ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45
 ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
 50 55 60
 caa tgc tgc agt ggc tgg tgc att ttc gcc tgc ctc taaaactgtc 238
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
 65 70 75
 gtgatgtctt ctcctccoct c 259

<210> 198
 <211> 76
 <212> PRT
 <213> Conus gloriamaris

<400> 198
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
 50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
 65 70 75

<210> 199
 <211> 24
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> SITE
 <222> (1)..(24)
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or bromo-Trp

<400> 199
 Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
 1 5 10 15

Gly Xaa Cys Ile Phe Ala Cys Leu
 20

<210> 200
 <211> 258
 <212> DNA
 <213> Conus dalli

<220>
 <221> CDS
 <222> (1)..(228)

<400> 200
 atg aaa ctg acg tgc att atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gcg ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gag gac tct gaa 144
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45

ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
 50 55 60

caa tgc tgc agt ggc tgg tgc att ttc gtc tgc ctc taaaactgcc 238
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu
 65 70 75

gtgatgtctt ctctcccatc 258

<210> 201
 <211> 76
 <212> PRT
 <213> Conus dalli

<400> 201
 Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu
65 70 75

<210> 202
<211> 24
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(24)
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
bromo-Trp

<400> 202
Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
1 5 10 15

Gly Xaa Cys Ile Phe Val Cys Leu
20

<210> 203
<211> 259
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(228)

<400> 203
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca gtc gtc acg gct gtg cct cac tcc aac aag cgg ttg gcg aat 96
Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn
20 25 30

ctt tat ctg aag gca cgt cac gaa atg aaa aac ccc gaa gcc tct aat 144
Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn
35 40 45

gtg gac aag agg tgc ttt gag agt tgg gta gct tgt gag tct cca aaa 192
Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
50 55 60

cga tgc tgc agt cac gtg tgc ctt ttc gtc tgc acc tgaaactgcc 238
Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
65 70 75

gtgatgtctt ctctctccct c 259

<400>	206															
atg	aaa	ctg	acg	tgt	atg	ttg	atc	atc	gct	gtg	ctg	ttc	ctg	acg	gcc	48
Met	Lys	Leu	Thr	Cys	Met	Leu	Ile	Ile	Ala	Val	Leu	Phe	Leu	Thr	Ala	
1				5					10					15		
tgt	caa	ctc	tct	aca	aat	gcg	agt	tac	gcc	aga	agt	aag	cag	aag	cat	96
Cys	Gln	Leu	Ser	Thr	Asn	Ala	Ser	Tyr	Ala	Arg	Ser	Lys	Gln	Lys	His	
			20					25					30			
cgt	gtt	ctg	agg	tcg	act	gac	aaa	aac	tcc	aag	ttg	acc	cag	cgt	tgc	144
Arg	Val	Leu	Arg	Ser	Thr	Asp	Lys	Asn	Ser	Lys	Leu	Thr	Gln	Arg	Cys	
		35					40					45				
aat	gaa	gct	caa	gaa	cat	tgc	act	caa	aat	cct	gac	tgc	tgc	agt	gag	192
Asn	Glu	Ala	Gln	Glu	His	Cys	Thr	Gln	Asn	Pro	Asp	Cys	Cys	Ser	Glu	

50 55 60

tct tgc aat aag ttt gtc ggc aga tgc ttg tca gac tgatctgatg 238
 Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 65 70 75

tcttctcctc ccatc 253

<210> 207
 <211> 76
 <212> PRT
 <213> Conus distans

<400> 207
 Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
 20 25 30
 Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
 35 40 45
 Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu
 50 55 60
 Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 65 70 75

<210> 208
 <211> 29
 <212> PRT
 <213> Conus distans

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 3, 6 and 17 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 12 may be Pro or hydroxy-Pro

<400> 208
 Cys Asn Xaa Ala Gln Xaa His Cys Thr Gln Asn Xaa Asp Cys Cys Ser
 1 5 10 15
 Xaa Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
 20 25

<210> 209
 <211> 259
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (1)..(228)

<400> 209
 atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gtg cct gac tcc agc aat gcg ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
 20 25 30

09749637.084394

<400> 212

ggcattacct aaaacatcac caag atg aaa ctg acg tgc atg atg atc gtt 51
 Met Lys Leu Thr Cys Met Met Ile Val
 1 5

gct gtg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gcg cct cac 99
 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Ala Pro His
 10 15 20 25

tcc agc aat gcg ttg gag aat ctt tat ctg aag gca cat cat gaa atg 147
 Ser Ser Asn Ala Leu Glu Asn Leu Tyr Leu Lys Ala His His Glu Met
 30 35 40

aac aac ccc gaa gcc tct gaa ttg aac aag agg tgc tat gat agt ggg 195
 Asn Asn Pro Glu Ala Ser Glu Leu Asn Lys Arg Cys Tyr Asp Ser Gly
 45 50 55

aca agt tgt aac act gga aac caa tgc tgc agt ggc tgg tgc att ttc 243
 Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp Cys Ile Phe
 60 65 70

gtc tct tgc ctc taaaactacc gtgatgtctt ctctcccct c 286
 Val Ser Cys Leu
 75

<210> 213
 <211> 77
 <212> PRT
 <213> Conus textile

<400> 213
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Ala Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Ala Ser Glu
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn
 50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Ser Cys Leu
 65 70 75

<210> 214
 <211> 25
 <212> PRT
 <213> Conus textile

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
 bromo-Trp

<400> 214
 Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
 1 5 10 15

Gly Xaa Cys Ile Phe Val Ser Cys Leu
 20 25

09749637 084304

<210> 215
 <211> 272
 <212> DNA
 <213> *Conus gloriamaris*

<220>
 <221> CDS
 <222> (1)..(252)

<400> 215
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ctg aca gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt 96
 Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30
 ttt tcg aaa tca cgt gac gaa atg gag gac ccc gaa gct tct aaa ttg 144
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
 35 40 45
 gag aaa agg gat tgc caa gca cta tgg gat tat tgt cca gta ccg ctc 192
 Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
 50 55 60
 ttg tca tcg ggt gat tgc tgc tat ggc tta atc tgt ggc cct ttc gtc 240
 Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val
 65 70 75 80
 tgc att gga tgg tga tgtcttc tactcccatc 272
 Cys Ile Gly Trp

<210> 216
 <211> 84
 <212> PRT
 <213> *Conus gloriamaris*

<400> 216
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
 35 40 45
 Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
 50 55 60
 Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val
 65 70 75 80
 Cys Ile Gly Trp

<210> 217
 <211> 33
 <212> PRT
 <213> *Conus gloriamaris*

<220>
 <221> SITE
 <222> (1)..(33)

<223> Xaa at residues 6 and 33 may be Trp or bromo-Trp; Xaa at residues 8 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 27 may be Pro or hydroxy-Pro

<400> 217

Asp Cys Gln Ala Leu Xaa Asp Xaa Cys Xaa Val Xaa Leu Leu Ser Ser
1 5 10 15

Gly Asp Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Ile Gly
20 25 30

Xaa

<210> 218

<211> 275

<212> DNA

<213> Conus omaria

<220>

<221> CDS

<222> (1)..(249)

<400> 218

atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc atg gct gat gac tcc aac aat gga ctg gca aat ctt 96
Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

ttc tcg aaa tca cgt gac gaa atg gag gat acc gat cct tct aaa ttg 144
Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
35 40 45

gag aac aga aaa act tgc caa aga agg tgg gat ttt tgt cca gga tcg 192
Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
50 55 60

ctc gtt gga gtg ata act tgc tgc ggt ggc tta atc tgt ttt ctg ttc 240
Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
65 70 75 80

ttc tgc gtt tgatagtgat gctcttctcc tcccct 275
Phe Cys Val

<210> 219

<211> 83

<212> PRT

<213> Conus omaria

<400> 219

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
35 40 45

Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
50 55 60

003746370301

Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
 65 70 75 80

Phe Cys Val

<210> 220

<211> 32

<212> PRT

<213> Conus omaria

<220>

<221> SITE

<222> (1)..(32)

<223> Xaa at residue 7 may be Trp or bromo-Trp; Xaa at residue 10 may be Pro or hydroxy-Pro

<400> 220

Lys Thr Cys Gln Arg Arg Xaa Asp Phe Cys Xaa Gly Ser Leu Val Gly
 1 5 10 15

Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe Phe Cys Val
 20 25 30

<210> 221

<211> 274

<212> DNA

<213> Conus dalli

<220>

<221> CDS

<222> (1)..(246)

<400> 221

atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ctg aca gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt 96
 Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30

ttt tcg aaa tta cgt gac gaa atg gag gac ccc gaa ggt tct aaa ttg 144
 Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
 35 40 45

gag aaa aag gat tgc caa gaa aaa tgg gat tat tgt cca gta ccg ttc 192
 Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
 50 55 60

ttg gga tcg agg tat tgc tgc gat ggc ttt atc tgt cca tct ttc ttc 240
 Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
 65 70 75 80

tgc gct tgatagtgat gtcttctcta ttcccctc 274
 Cys Ala

<210> 222

<211> 82

<212> PRT

<213> Conus dalli

<400> 222

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
 20 25 30

Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
 35 40 45

Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
 50 55 60

Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
 65 70 75 80

Cys Ala

<210> 223

<211> 31

<212> PRT

<213> Conus dalli

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residues 8 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 26 may be Pro or hydroxy-Pro

<400> 223

Asp Cys Gln Xaa Lys Xaa Asp Xaa Cys Xaa Val Xaa Phe Leu Gly Ser
 1 5 10 15

Arg Xaa Cys Cys Asp Gly Phe Ile Cys Xaa Ser Phe Phe Cys Ala
 20 25 30

<210> 224

<211> 271

<212> DNA

<213> Conus dalli

<220>

<221> CDS

<222> (1)..(252)

<400> 224

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ttg ttc ctg aca gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat cat 96
 Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
 20 25 30

ttt tgg aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg 144
 Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
 35 40 45

gag aaa agg gat tgc caa ggc gaa tgg gag ttt tgt ata gta ccg gtc 192
 Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
 50 55 60

ctt gga ttt gtg tat tgc tgc ccc tgg ctt atc tgt ggc cct ttc gtc 240
 Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
 65 70 75 80

102120 436460

tgc gtt gat atc tgatgtcttc tatccctc
Cys Val Asp Ile

271

<210> 225
<211> 84
<212> PRT
<213> Conus dalli

<400> 225
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

Cys Val Asp Ile

<210> 226
<211> 33
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(33)
<223> Xaa at residues 5 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 6 and 22 may be Trp or bromo-Trp; Xaa at residues 12, 21
and 27 may be Pro or hydroxy-Pro;

<220>
<221> SITE
<222> (1)..(33)
<223> Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-T
yr, O-sulpho-Tyr or O-phospho-Tyr

<400> 226
Asp Cys Gln Gly Xaa Xaa Phe Cys Ile Val Xaa Val Leu Gly Phe
1 5 10 15

Val Xaa Cys Cys Xaa Xaa Leu Ile Cys Gly Xaa Phe Val Cys Val Asp
20 25 30

Ile

<210> 227
<211> 265
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(234)

<400> 227
atg aaa ctg acg tgc ctg atg atc att gct gtg ctg ttc ttg acc gcc

48

004937 004937

Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc atg gct gat gac ccc aga gat gaa ccg gag gca cgt 96
 Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
 20 25 30

gac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc tgc ctt 144
 Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
 35 40 45

gaa gtt gat tat ttt tgc ggc ata ccg ttt gtg aac aac ggg cta tgc 192
 Glu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys
 50 55 60

tgc agt ggc aat tgt gtt ttt gtc tgc aca ccc caa ggg aag 234
 Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
 65 70 75

taaaaactgct gtgatgtctt ctcttcccat c 265

<210> 228
 <211> 78
 <212> PRT
 <213> Conus pennaceus

<400> 228
 Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
 20 25 30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
 35 40 45

Glu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys
 50 55 60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
 65 70 75

<210> 229
 <211> 31
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue
 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydrox
 y-Pro

<400> 229
 Gly Cys Leu Xaa Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
 1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
 20 25 30

<210> 230
 <211> 428

09749637.081301

<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (122)..(229)

<400> 230
ggtcgacatc atcatcatcg atccatctgt ccatccatct gtccatccat ccattcattc 60
attcactgcc aaactgtcat aaatatattga gtctctcttt ctgtttttat ctgacagatt 120
g aac gag aga gac tgc ctt aat gtt gat tat ttt tgc ggc ata ccg ttt 169
Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15
gtg aac aac ggg cta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca 217
Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30
ccc caa ggg aag taaaactgcc gtgatgtctt ctcttcccct ctagtagtag 269
Pro Gln Gly Lys
35
taggcggccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt 329
ctatagtgtc acctaaattc aattcactgg ccgtccgttt tacaacgtcg tgactgggaa 389
aaccctggcg ttaccaact taatgcctt gcagcacat 428

<210> 231
<211> 36
<212> PRT
<213> Conus marmoreus

<400> 231
Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15
Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30
Pro Gln Gly Lys
35

<210> 232
<211> 30
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residue 6 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 11 and 29 may be Pro or hydroxy-Pro

<400> 232
Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn Gly
1 5 10 15
Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
20 25 30

<210> 233
 <211> 227
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (105)..(224)

<400> 233
 tcgacatcat catcatcgat ccatctgtcc atccatccat tcattcattc gctgccaaac 60
 tgtcataaat atttgagtct ctctttctgt ttttatctga caga ttg gac aag aga 116
 Leu Asp Lys Arg
 1

gag tgc ctg gaa gct gat tat tat tgc gtc tta ccg ttt gtg ggc aac 164
 Glu Cys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro Phe Val Gly Asn
 5 10 15 20

ggg atg tgc tgc agt ggc att tgt gtt ttt gtc tgc ata gcc caa cgc 212
 Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
 25 30 35

ttt aaa acc gtc tga 227
 Phe Lys Thr Val
 40

<210> 234
 <211> 40
 <212> PRT
 <213> Conus marmoreus

<400> 234
 Leu Asp Lys Arg Glu Cys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro
 1 5 10 15
 Phe Val Gly Asn Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys
 20 25 30
 Ile Ala Gln Arg Phe Lys Thr Val
 35 40

<210> 235
 <211> 36
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> SITE
 <222> (1)..(36)
 <223> Xaa at residues 1 and 4 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidues 7 and 8 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr
 , O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 12 may be Pro or
 hydroxy-Pro

<400> 235
 Xaa Cys Leu Xaa Ala Asp Xaa Xaa Cys Val Leu Xaa Phe Val Gly Asn
 1 5 10 15
 Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
 20 25 30
 Phe Lys Thr Val

35

<210> 236
 <211> 525
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (131)..(241)

<400> 236
 gtaccggtcc ggaattcccg ggtcgacatc atcatcatcg atccatctgt ccatccatcc 60
 atccattcat tcattcgctg ccaaactgtc ataaacattt gagtctctct ttctgttttt 120
 atctgacaga ttg aac gag aga gac tgc ctt gaa cct gat tat gtt tgc 169
 Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys
 1 5 10
 ggc ata ccg ttt gtg ttc aac ggg cta tgc tgc agt gga att tgt gtt 217
 Gly Ile Pro Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val
 15 20 25
 ttt atc tgc ata gcc caa aag tat taaaacgccg tgatgtcttc tattcccatc 271
 Phe Ile Cys Ile Ala Gln Lys Tyr
 30 35
 tagtagtagt aggcggccgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc 331
 atagctcttc tatagtgtca cctaaattca attcactggc cgtcgtttta caacgtcgtg 391
 actgggaaaa ccttggcggtt acccaactta atcgcccttg agcacatccc cctttcgcca 451
 gctggcgtaa tagccgaaga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg 511
 aatggcgaat gggg 525

<210> 237
 <211> 37
 <212> PRT
 <213> Conus marmoreus

<400> 237
 Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys Gly Ile Pro
 1 5 10 15
 Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys
 20 25 30
 Ile Ala Gln Lys Tyr
 35

<210> 238
 <211> 33
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> SITE
 <222> (1)..(33)
 <223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residues
 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 33 may
 be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O

-phospho-Tyr

<400> 238

Asp Cys Leu Xaa Xaa Asp Xaa Val Cys Gly Ile Xaa Phe Val Phe Asn
 1 5 10 15

Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys Ile Ala Gln Lys
 20 25 30

Xaa

<210> 239

<211> 537

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (146)..(247)

<400> 239

ggtacgcctg caggtaccgg tccggaattc ccgggtcgac atcatcatca tcatcgatcc 60

atctgtccat ccattctattc attcattogc tgtcaaactg taatacatat tagaatctct 120

ctttctgttt gtattctgaca gattg gag aaa agg gcg tgc agc aaa aaa tgg 172
 Glu Lys Arg Ala Cys Ser Lys Lys Trp
 1 5

gaa tat tgt ata gta ccg atc ott gga ttc gta tat tgc tgc cct ggc 220
 Glu Tyr Cys Ile Val Pro Ile Leu Gly Phe Val Tyr Cys Cys Pro Gly
 10 15 20 25

tta atc tgt ggt cct ttc gtc tgc gtt tgatagtgat gtcttctcct 267
 Leu Ile Cys Gly Pro Phe Val Cys Val
 30

cccatctagt agtagtaggc ggccgctcta gaggatccaa gcttacgtac gcgtgcatgc 327

gacgtcatag ctcttctata gtgtcaccta aattcaattc actggccgtc gttttacaac 387

gtcgtgactg ggaaaaccct ggcgttaccc aacttaatcg ccttgcagca catccccctt 447

tcgccagctg gcgtaataag cgaagaggcc cgcaccgatc gcccttccca acagttgcgc 507

agcctgaatg gcgaaatggg acgcgccttg 537

<210> 240

<211> 34

<212> PRT

<213> Conus marmoreus

<400> 240

Glu Lys Arg Ala Cys Ser Lys Lys Trp Glu Tyr Cys Ile Val Pro Ile
 1 5 10 15

Leu Gly Phe Val Tyr Cys Cys Pro Gly Leu Ile Cys Gly Pro Phe Val
 20 25 30

Cys Val

<210> 241

<211> 31

<212> PRT

094967 0340

<213> Conus marmoreus

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 8 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 21 and 27 may be Pro or hydroxy-Pro

<400> 241

Ala Cys Ser Lys Lys Xaa Xaa Xaa Cys Ile Val Xaa Ile Leu Gly Phe
1 5 10 15

Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val
20 25 30

<210> 242

<211> 552

<212> DNA

<213> Conus omaria

<220>

<221> CDS

<222> (149)..(271)

<400> 242

aaagccggta cgctgcagg taccgggtccg gaattcccgg gtcgacatca tcatcatcat 60

cgatccatct gtccatccat ccattcattc attcactgcc aaactgtcat aaatatttga 120

gtctctcttt ctgtttttat ctgacaga ttg aac gag aga gac tgc ctt aat 172
Leu Asn Glu Arg Asp Cys Leu Asn
1 5

gtt gat tat ttt tgt ggc ata ccg ttt gtg aac aac ggg cta tgc tgc 220
Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys
10 15 20

agt ggc aat tgt gtt ttt tgt ctg cac acc cca agg gaa gta aaa ctg 268
Ser Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu
25 30 35 40

ccg tgatgtcttc tcttcccttc tagtagtagt aggcggccgc tctagaggat 321
Pro

ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca cctaaattca 381

attcactggc cgctgtttta caacgtcgtg actgggaaaa cctggcggtt acccaactta 441

atcgcccttg agcacatccc ctttgcgcca gctggcgtaa tagcgaagag gcccgaccg 501

atcgcccttc ccaacagttg cgcagcctga atggcgaatg ggacgcgccc t 552

<210> 243

<211> 41

<212> PRT

<213> Conus omaria

<400> 243

Leu Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro
1 5 10 15

Phe Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu
 20 25 30

His Thr Pro Arg Glu Val Lys Leu Pro
 35 40

<210> 244

<211> 37

<212> PRT

<213> Conus omaria

<220>

<221> SITE

<222> (1)..(37)

<223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 31 and 37 may be Pro or hydroxy-Pro; Xaa at residue 33 may be Glu or gamma-carboxy-Glu

<400> 244

Asp Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
 1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu His Thr Xaa Arg
 20 25 30

Xaa Val Lys Leu Xaa
 35

<210> 245

<211> 212

<212> DNA

<213> Conus obscurus

<220>

<221> CDS

<222> (86)..(181)

<400> 245

cgatccatct gtccatccat ccattcattc attcattgcc aaactgtaac aaatattcaa 60

gtctctcttt ctgtttgtgt ctgac aga tcg aaa cgg tgc ctt gtt tac ggt 112
 Arg Ser Lys Arg Cys Leu Val Tyr Gly
 1 5

aca cct tgt gac tgg ctg acc att gcg ggt atg gag tgc tgc agt aaa 160
 Thr Pro Cys Asp Trp Leu Thr Ile Ala Gly Met Glu Cys Cys Ser Lys
 10 15 20 25

aag tgc ttt atg atg tgc tgg taaaactgcc gtgatgtott ctactcccct c 212
 Lys Cys Phe Met Met Cys Trp
 30

<210> 246

<211> 32

<212> PRT

<213> Conus obscurus

<400> 246

Arg Ser Lys Arg Cys Leu Val Tyr Gly Thr Pro Cys Asp Trp Leu Thr
 1 5 10 15

Ile Ala Gly Met Glu Cys Cys Ser Lys Lys Cys Phe Met Met Cys Trp
 20 25 30

0944037 084304

<210> 247
 <211> 28
 <212> PRT
 <213> Conus obscurus

<220>
 <221> SITE
 <222> (1)..(28)
 <223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residues 10 and 28 may be Trp or bromo-Trp; Xaa at residue 17 may be Glu or gamma-carboxy-Glu

<400> 247
 Cys Leu Val Xaa Gly Thr Xaa Cys Asp Xaa Leu Thr Ile Ala Gly Met
 1 5 10 15
 Xaa Cys Cys Ser Lys Lys Cys Phe Met Met Cys Xaa
 20 25

<210> 248
 <211> 139
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (2)..(109)

<400> 248
 a ttg aac cag aga gac tgc cat gaa gtt ggt gaa ttt tgt ggc tta ccg 49
 Leu Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
 1 5 10 15
 tta ata aag aac ggg cta tgc tgc agt cag att tgt tta ggt gtc tgc 97
 Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
 20 25 30
 gca aaa gtg ttt taaaactgcc gtgatgtctt ctactcccat 139
 Ala Lys Val Phe
 35

<210> 249
 <211> 36
 <212> PRT
 <213> Conus radiatus

<400> 249
 Leu Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
 1 5 10 15
 Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
 20 25 30
 Ala Lys Val Phe
 35

<210> 250
 <211> 32
 <212> PRT
 <213> Conus radiatus

<220>
 <221> SITE

<222> (1)..(32)

<223> Xaa at residues 4 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydroxy-Pro

<400> 250

Asp Cys His Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
1 5 10 15

Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys Ala Lys Val Phe
20 25 30

<210> 251

<211> 133

<212> DNA

<213> Conus radiatus

<220>

<221> CDS

<222> (2)..(100)

<400> 251

a tta gac aag aaa gag tgc act gcc aat ggt gaa ttt tgt ggc ata tcg 49
Leu Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

gtc ttt gga agc tac cta tgc tgc agt ggc cgg tgt gta ttc gtc tgc 97
Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
20 25 30

atc tagttgaact gccgtgatgt cttctactcc cct 133
Ile

<210> 252

<211> 33

<212> PRT

<213> Conus radiatus

<400> 252

Leu Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
20 25 30

Ile

<210> 253

<211> 29

<212> PRT

<213> Conus radiatus

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 253

Xaa Cys Thr Ala Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser
1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys Ile
20 25

094037 034460

<210> 254
 <211> 133
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (2)..(100)

<400> 254
 a ttg gac aag aaa gag tgc act acc aat ggt gaa ttt tgt ggc ata tcg 49
 Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
 1 5 10 15
 gtc ttt gca agc ttc cta tgc tgc agt ggc ctg tgt gta ttc gtc tgc 97
 Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
 20 25 30
 atc tagctgaact gccgtgatgt cttctcttcc cct 133
 Ile

<210> 255
 <211> 33
 <212> PRT
 <213> Conus radiatus

<400> 255
 Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
 1 5 10 15
 Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
 20 25 30
 Ile

<210> 256
 <211> 29
 <212> PRT
 <213> Conus radiatus

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu.

<400> 256
 Xaa Cys Thr Thr Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Ala Ser
 1 5 10 15
 Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys Ile
 20 25

<210> 257
 <211> 133
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (2)..(100)

<400> 257
 a ttg gac aag aga aaa tgc ttt ccc aaa aat cat ttt tgt ggc ttt gtg 49
 Leu Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val

00749637 00304

1 5 10 15

gtg atg ctg aac tac cta tgc tgc agt ggc cgg tgt ata ttc gtc tgc 97
 Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
 20 25 30

gtc tagttgaact gccgtgatgt cttctactcc cat 133
 Val

<210> 258
 <211> 33
 <212> PRT
 <213> Conus radiatus

<400> 258
 Leu Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val
 1 5 10 15
 Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
 20 25 30
 Val

<210> 259
 <211> 29
 <212> PRT
 <213> Conus radiatus

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 17 may
 be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
 -phospho-Tyr

<400> 259
 Lys Cys Phe Xaa Lys Asn His Phe Cys Gly Phe Val Val Met Leu Asn
 1 5 10 15
 Xaa Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys Val
 20 25

<210> 260
 <211> 130
 <212> DNA
 <213> Conus regius

<220>
 <221> CDS
 <222> (1)..(99)

<400> 260
 ttg aac aag aga agc tgc ctt cct cta gac tgg ttt tgt ggc ttc aat 48
 Leu Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn
 1 5 10 15
 ata att gga gcg ttt ctg tgc tgt agt ggc tac tgc ctt gtc gtc tgc 96
 Ile Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
 20 25 30
 atg taaaactgcc gtgatgtctt ctctcccct c 130
 Met

<210> 261

<211> 33
 <212> PRT
 <213> Conus regius

<400> 261
 Leu Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn
 1 5 10 15
 Ile Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
 20 25 30

Met

<210> 262
 <211> 29
 <212> PRT
 <213> Conus regius

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Trp or bromo-Trp; Xaa at residue 23 may be Tyr, 125-I-Tyr, mon o-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 262
 Ser Cys Leu Xaa Leu Asp Xaa Phe Cys Gly Phe Asn Ile Ile Gly Ala
 1 5 10 15
 Phe Leu Cys Cys Ser Gly Xaa Cys Leu Val Val Cys Met
 20 25

<210> 263
 <211> 319
 <212> DNA
 <213> Conus delessertii

<220>
 <221> CDS
 <222> (1)..(285)

<400> 263
 atg aaa ctg acg tgt ctg ctg atc gtt gct gtg ctg gtc ttg gca gcc 48
 Met Lys Leu Thr Cys Leu Leu Ile Val Ala Val Leu Val Leu Ala Ala
 1 5 10 15
 tgt cag ttc atc gta gct ggc gac tcg agt gat ggc cag gag aat cct 96
 Cys Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro
 20 25 30
 gct ctg agg tca cct agc gat tcc tct ggg aaa atg tca tca atg aag 144
 Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys
 35 40 45
 cgc ttc cag aca cgg ctg atg gtg ggg caa tct gca tcg aaa aga cca 192
 Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
 50 55 60
 agc aag agg gac tgc atc ccc ggc ggc gaa aat tgt gat gta ttc cga 240
 Ser Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
 65 70 75 80
 cca tac cgg tgc tgc agt gga tat tgc ata cta ctc ctt tgc gca 285
 Pro Tyr Arg Cys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala

09749637.001301

85

90

95

tgataaaagct gcottgatgt cttctcctcc cctc

319

<210> 264

<211> 95

<212> PRT

<213> Conus delessertii

<400> 264

Met	Lys	Leu	Thr	Cys	Leu	Leu	Ile	Val	Ala	Val	Leu	Val	Leu	Ala	Ala
1				5					10					15	

Cys	Gln	Phe	Ile	Val	Ala	Gly	Asp	Ser	Ser	Asp	Gly	Gln	Glu	Asn	Pro
			20					25					30		

Ala	Leu	Arg	Ser	Pro	Ser	Asp	Ser	Ser	Gly	Lys	Met	Ser	Ser	Met	Lys
		35					40					45			

Arg	Phe	Gln	Thr	Arg	Leu	Met	Val	Gly	Gln	Ser	Ala	Ser	Lys	Arg	Pro
	50					55					60				

Ser	Lys	Arg	Asp	Cys	Ile	Pro	Gly	Gly	Glu	Asn	Cys	Asp	Val	Phe	Arg
65					70					75					80

Pro	Tyr	Arg	Cys	Cys	Ser	Gly	Tyr	Cys	Ile	Leu	Leu	Leu	Cys	Ala
			85						90					95

<210> 265

<211> 28

<212> PRT

<213> Conus delessertii

<220>

<221> SITE

<222> (1)..(28)

<223> Xaa at residues 4 and 14 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 15 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 265

Asp	Cys	Ile	Xaa	Gly	Gly	Xaa	Asn	Cys	Asp	Val	Phe	Arg	Xaa	Xaa	Arg
1				5					10					15	

Cys	Cys	Ser	Gly	Xaa	Cys	Ile	Leu	Leu	Cys	Ala
			20				25			

<210> 266

<211> 1009

<212> DNA

<213> Conus striatus

<220>

<221> CDS

<222> (147)..(233)

<220>

<221> misc_feature

<222> (1)..(1009)

<223> n may be any nucleotide

<400> 266

gctgggttcgc ctgcaggtac cgggtccggaa ttcccgggtc gacatcatca tcatcgtacc

60

09240637.061301

atctgtccat ccactctatc attcattcat tcgctgccaa actgtattaa atattcaagt 120

ctctctttct gtttgtgtct aacaga ttg aga tgg tgc att cct agt ggt gaa 173
 Leu Arg Trp Cys Ile Pro Ser Gly Glu
 1 5

ctt tgt ttc cgc tgc gat cac ata gga tgc tgc agt ggc aag tgc gca 221
 Leu Cys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala
 10 15 20 25

ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctcccat ctagtagtag 273
 Phe Val Cys Leu

taggcggccg ctctagagga tccaagctta cgtacgogtg catgcgacgt catagctott 333

ctatagtgtc acctaaattc aattcactgg cgtcggtttt acaacgtcgt gactgggaaa 393

accctggcgt taccctaaatt aatcgctttg cagcacatcc ccctttcgcc agctggcgta 453

atagcgaaga ggcccgccac gatcgccctt cccaacagtt tgcgcagcct gaatggcgaa 513

tgggaacgcg cctgtagcgg cgcattaaac cgcggcgggt gtgggtgggt tacgcccacg 573

tgaccgcgta caettgccag cgccttancg ccccgctcct ttcgctttct ttcccttctt 633

ttctcgncac gtttcggccg nttttcccg tcaagctctt aaatcggggg gcttcccttt 693

aagggttnc gaattantgc ttaccgna cccttgaccc ccaaaaaaac ttggantaag 753

ggngatggn tncgtaant gggggccatc nccctgaan agaacggttt ttcnccctt 813

ttgacngttg ggngttcnc gggttttaaa aaangggacc tttntttcc aaaactggga 873

ananacctaa accctatttt tggggctatt ttttgantt tnaaangga ttttgcccca 933

ttttnggcc tnttggggta aaaaaagag ccggttttaa aaaaaatttt accccaaatt 993

ttaacaaaaa tttttt 1009

<210> 267
 <211> 29
 <212> PRT
 <213> Conus striatus

<400> 267
 Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys Phe Arg Ser Asp His
 1 5 10 15
 Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 268
 <211> 29
 <212> PRT
 <213> Conus striatus

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residue3 may be Trp or bromo-Trp; Xaa at residue 6 may be
 Pro or hydroxy-Pro; Xaa at residue 9 may be Glu or gamma-carboxy
 -Glu

09749637.081304

<400> 268

Leu Arg Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Phe Arg Ser Asp His
 1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 269

<211> 90

<212> DNA

<213> Conus striatus

<220>

<221> CDS

<222> (1)..(87)

<400> 269

ttg aga tgg tgc att cct agt ggt gat ctt tgt ttc cgc tcg gat cac 48
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
 1 5 10 15

ata gga tgc tgc agt ggc aag tgc gca ttc gtc tgc ttg taa 90
 Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 270

<211> 29

<212> PRT

<213> Conus striatus

<400> 270

Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
 1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 271

<211> 27

<212> PRT

<213> Conus striatus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be Pro or hydroxy-Pro

<400> 271

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gly
 1 5 10 15

Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 272

<211> 90

<212> DNA

<213> Conus striatus

<220>

<221> CDS

<222> (1)..(87)

T05480 2E95460

<400> 272
 ttg aga tgg tgc att cct agt ggt gat ctt tgt ttc cgc tcg gat cac 48
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
 1 5 10 15

ata caa tgc tgc agt ggc aag tgc gca ttc gtc tgc ttg taa 90
 Ile Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 273
 <211> 29
 <212> PRT
 <213> Conus striatus

<400> 273
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
 1 5 10 15
 Ile Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 274
 <211> 27
 <212> PRT
 <213> Conus striatus

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue1 may be Trp or bromo-Trp; Xaa at residue 4 may be
 Pro or hydroxy-Pro

<400> 274
 Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gln
 1 5 10 15
 Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 275
 <211> 206
 <212> DNA
 <213> Conus obscurus

<220>
 <221> CDS
 <222> (77)..(175)

<400> 275
 cgatecatct gtccatccat ccatttcagtc attcgtctgcc aaactgtaac aaatattcaa 60
 gtctttgcttt ctgttt gtg tct gac aga ttg aga tgg tgc gtt cct agc ggt 112
 Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly
 1 5 10

gaa gtt tgt cgc cgc tat gaa ttc gtg gga tgc tgc agt ggc aag tgc 160
 Glu Val Cys Arg Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys
 15 20 25

ttc ttc gtc tgc tcg taaaaactgtt gtgatgtctt ctctccct c 206
 Phe Phe Val Cys Ser
 30

<210> 276

0974567.004304

<211> 33
 <212> PRT
 <213> Conus obscurus

<400> 276
 Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly Glu Val Cys Arg
 1 5 10 15
 Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys
 20 25 30

Ser

<210> 277
 <211> 29
 <212> PRT
 <213> Conus obscurus

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residue 3 may be Trp or bromo-Trp; Xaa at residue 6 may be
 Pro or hydroxy-Pro; Xaa at residues 9 and 15 may be Glu or gamma
 -carboxy-Glu; Xaa at residue 14 may be Tyr, 125-I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 277
 Leu Arg Xaa Cys Val Xaa Ser Gly Xaa Val Cys Arg Arg Xaa Xaa Phe
 1 5 10 15
 Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys Ser
 20 25

<210> 278
 <211> 259
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (22)..(117)

<400> 278
 ctctctctct ctctgctgga c agg tgc act cgc tgc ttg cct gac gga acg 51
 Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr
 1 5 10
 tct tgc ctt ttt agt agg atc aga tgc tgc ggt act tgc agt tca atc 99
 Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile
 15 20 25
 tta aag tca tgt gtg agc tgatccggcg gttgatcttc ctccctctgt 147
 Leu Lys Ser Cys Val Ser
 30
 gctccatcct tttctgctg agtccctcctt acctgagagt ggatcatgaac cactcatcac 207
 ctactcctct ggaggcttca gaggagctac attgaaataa aagccgcatt gc 259

<210> 279
 <211> 32
 <212> PRT
 <213> Conus radiatus

T00180-2E954250

tctgggggcc tcgggggttc aacatccaaa taaagcgaca acacaatcac aagtaaaaaa 478

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<400> 284
gc tgc agg tcg act cta gag gcg ttg gag aat ctt tat ctg aag gca      47
  Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala
   1          5          10          15

cat cat gaa atg aac aac ccc gaa gac tct gaa ttg aac aag agg tgc      95
His His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys
      20          25          30

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tat gat agt ggg aca agt tgt aac act gga aac caa tgc tgc agt ggc 143
 Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly
 35 40 45

tgg tgc att ttc gtc tgc ctc taaaactgcc gtgatgtctt ctactccct 194
 Trp Cys Ile Phe Val Cys Leu
 50

ctgtgctacc tacctggctt gatctttgat tggcgcgtgc ccttcaactgg ttatgaaccc 254

ctctgatccg actctctggg ggccctcgggg atccaacatc aaaatanagc gacagcacia 314

tcac 318

<210> 285

<211> 54

<212> PRT

<213> Conus textile

<400> 285

Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala His
 1 5 10 15

His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys Tyr
 20 25 30

Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp
 35 40 45

Cys Ile Phe Val Cys Leu
 50

<210> 286

<211> 24

<212> PRT

<213> Conus textile

<220>

<221> SITE

<222> (1)..(24)

<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
 bromo-Trp

<400> 286

Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
 1 5 10 15

Gly Xaa Cys Ile Phe Val Cys Leu
 20

<210> 287

<211> 480

<212> DNA

<213> Conus quercinus

<220>

<221> CDS

<222> (52)..(333)

<400> 287

gcttcgtatt tctccgctgt cttccttggc atcaccacaaa acatcaccaa g atg aaa
 Met Lys
 1

57

ctg acg tgc atg atg atc gtt gct ctg ctg ttc ttg acc gcc tgg aca 105
 Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala Trp Thr
 5 10 15

ttc gtc acg gct gtt gac tcc aaa aat gaa ctg gag aac aga gga gga 153
 Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg Gly Gly
 20 25 30

tgg ggg cag gca gga gga tgg ggg aaa ctt ttt ccg atg gca cgc gac 201
 Trp Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala Arg Asp
 35 40 45 50

gaa atg aaa aac agc gaa gtc tct aaa ttg gac aat aag aga aag tgc 249
 Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg Lys Cys
 55 60 65

gct gca gcc ggt gaa gct tgc gta ata cct atc att gga aac gta ttt 297
 Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn Val Phe
 70 75 80

tgc tgc aaa ggc tac tgt ctt ttc gtc tgc att agt taaactgctg 343
 Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser
 85 90

tgatgccttc tactcacctc tgtgctacct ggcttgatct ttgattggcg tgtgcccttc 403

actggttatg agctcgctcg atcctactct ctggagacct ctgtggtcca acatccaaat 463

aaagcggcat cccaatg 480

<210> 288
 <211> 94
 <212> PRT
 <213> Conus quercinus

<400> 288
 Met Lys Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg
 20 25 30

Gly Gly Trp Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala
 35 40 45

Arg Asp Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg
 50 55 60

Lys Cys Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn
 65 70 75 80

Val Phe Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser
 85 90

<210> 289
 <211> 29
 <212> PRT
 <213> Conus quercinus

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 11 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tyr, 125-I

-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 289

Cys Ala Ala Ala Gly Xaa Ala Cys Val Ile Xaa Ile Ile Gly Asn Val
1 5 10 15

Phe Cys Cys Lys Gly Xaa Cys Leu Phe Val Cys Ile Ser
20 25

<210> 290

<211> 410

<212> DNA

<213> Conus leopardus

<220>

<221> CDS

<222> (1)..(246)

<400> 290

atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg ata ttc atc acg gct gat gac tcc aca aat gga ctg gag aat cgt 96
Trp Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg
20 25 30

ttt agg aag gca cgt gac aac atg aag aac gcc aaa gcc tct aca tta 144
Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
35 40 45

gcc gag aag aaa gcg tgt gtt gaa ctt ggt gag att tgt gcc aca gcc 192
Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly
50 55 60

ttc ttc cta gac gag gaa tgc tgc act ggt tca tgc cat gtc ttc tgc 240
Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
65 70 75 80

gta cta tagttaaact gctgtgatgt cttcttctct cctccgtgct acctggcttg 296
Val Leu

atcttttgatt ggtgcctgtc cttcagtggt tgtgaaaccc tctgatccta ctctctggac 356

gcctctgagg cccaacatcc aaataaagcg acatcctaata gccaaaaaaa aaaa 410

<210> 291

<211> 82

<212> PRT

<213> Conus leopardus

<400> 291

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg
20 25 30

Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
35 40 45

Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly
50 55 60

Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
65 70 75 80

Val Leu

<210> 292

<211> 30

<212> PRT

<213> Conus leopardus

<220>

<221> SITE

<222> (1)..(30)

<223> Xaa at residues 4, 7, 17 and 18 may be Glu or gamma-carboxy-Glu.

<400> 292

Ala Cys Val Xaa Leu Gly Xaa Ile Cys Ala Thr Gly Phe Phe Leu Asp
1 5 10 15

Xaa Xaa Cys Cys Thr Gly Ser Cys His Val Phe Cys Val Leu
20 25 30

<210> 293

<211> 336

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (1)..(231)

<400> 293

atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

ttt tgc aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt gaa caa 192
Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
50 55 60

aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta taaaactacc 241
Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

gtgatgtcctt ctactcccct ctgtgctgcc tggcttgatc tttgattggc gcgtgccctt 301

cactggttat gacccccctg atccgacctc tggggg 336

<210> 294

<211> 77

<212> PRT

<213> Conus marmoreus

<400> 294

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala

094567-081301

1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60
 Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
 65 70 75

<210> 295
 <211> 26
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and
 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 ma
 y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

<400> 295
 Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
 1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
 20 25

<210> 296
 <211> 402
 <212> DNA
 <213> Conus quercinus

<220>
 <221> CDS
 <222> (7)..(240)

<400> 296
 ggatcc atg aaa ctg acg tgt atg gtg atc gtt gct gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gcc tcg gct gat gac tcc aga aat gga ttc gag aat cga aat gga 96
 Thr Ala Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly
 15 20 25 30

gaa cga aac gaa aac gaa atg aag aac ctc gaa gcc tct aaa ttg aac 144
 Glu Arg Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn
 35 40 45

agg aga gac ggc gat tgc gtt gat ggt ggt gaa ttt tgt ggc ttt ccg 192
 Arg Arg Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro
 50 55 60

aaa att gga ggg cca tgc tgt agt ggc tgg tgc ttt ttc gtc tgc tta 240
 Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

taaaactgcc atgatgtctt ctacccccct ctgtgctacc tgacttgatc tttgattggc 300
 gtgtgccctt cactgggtat gaacccctct gatccgactc tctggaggcc tcgggggtcc 360
 aacatccaaa taaagcgaca gcaaaaaaaaa aaaaaaaaaa aa 402

<210> 297
 <211> 78
 <212> PRT
 <213> Conus quercinus

<400> 297
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly Glu Arg
 20 25 30
 Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn Arg Arg
 35 40 45
 Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro Lys Ile
 50 55 60
 Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

<210> 298
 <211> 30
 <212> PRT
 <213> Conus quercinus
 <220>
 <221> SITE
 <222> (1)..(30)
 <223> Xaa at residue 9 may be Glu or gamma-carboxy-Glu; Xaa at residues
 14 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp
 or bromo-Trp

<400> 298
 Asp Gly Asp Cys Val Asp Gly Gly Xaa Phe Cys Gly Phe Xaa Lys Ile
 1 5 10 15
 Gly Gly Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
 20 25 30

<210> 299
 <211> 274
 <212> DNA
 <213> Conus quercinus

<220>
 <221> CDS
 <222> (7)..(216)

<220>
 <221> misc_feature
 <222> (1)..(274)
 <223> n may be any nucleotide

<400> 299
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gcc ttg gct gat gac tcc aga aat gga ttg gag aat cga aat gaa 96
 Thr Ala Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu
 15 20 25 30

caa gaa cga aac gaa aac gaa atg agg gac cgc cgg gac tgc caa gat 144
 Gln Glu Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp
 35 40 45

agt ggt gta gtt tgt ggc ttt ccg aaa cct gaa cca cac tgc tgc agt 192
 Ser Gly Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser
 50 55 60

ggc tgg tgc ctt ttc gtc tgc gcc taaaactgcc gtgatgtcaa ataaagcgac 246
 Gly Trp Cys Leu Phe Val Cys Ala
 65 70

agacaatnaa aaaaaaaaaa aaaaaaaaaa 274

<210> 300
 <211> 70
 <212> PRT
 <213> Conus quercinus

<400> 300
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu Gln Glu
 20 25 30

Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp Ser Gly
 35 40 45

Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser Gly Trp
 50 55 60

Cys Leu Phe Val Cys Ala
 65 70

<210> 301
 <211> 28
 <212> PRT
 <213> Conus quercinus

<220>
 <221> SITE
 <222> (1)..(28)
 <223> Xaa at residues 12, 14 and 16 may be Pro or hydroxy-Pro; Xaa at r
 esidue15 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may b
 e Trp or bromo-Trp

<400> 301
 Asp Cys Gln Asp Ser Gly Val Val Cys Gly Phe Xaa Lys Xaa Xaa Xaa
 1 5 10 15

His Cys Cys Ser Gly Xaa Cys Leu Phe Val Cys Ala
 20 25

<210> 302
 <211> 340
 <212> DNA
 <213> Conus arenatus

<220>

00465460

<221> CDS
 <222> (7)..(246)

<220>
 <221> misc_feature
 <222> (1)..(340)
 <223> n may be any nucleotide

<400> 302
 ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gcc tgg aca ttc gtc acg gct gac tcc ata cgt gca ctg gag gat 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp
 15 20 25 30

ttt ttt gcg aag gca cgt gac gaa atg gaa aac agc gga gct tct cca 144
 Phe Phe Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro
 35 40 45

ttg aac gag aga gac tgc cga cct gta ggt caa tat tgt ggc ata ccg 192
 Leu Asn Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro
 50 55 60

tat aag cac aac tgg cga tgc tgc agt cag ctt tgt gca att atc tgt 240
 Tyr Lys His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys
 65 70 75

gtt tcc taacccctct gatcctactc tctgaagacc tccgggattc aacatccaaa 296
 Val Ser
 80

taaagcgaca tcccgatnaa aaaaaangaa aaaaaaaaaa aaaa 340

<210> 303
 <211> 80
 <212> PRT
 <213> Conus arenatus

<400> 303
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp Phe Phe
 20 25 30
 Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro Leu Asn
 35 40 45
 Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro Tyr Lys
 50 55 60
 His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
 65 70 75 80

<210> 304
 <211> 30
 <212> PRT
 <213> Conus arenatus

<220>
 <221> SITE
 <222> (1)..(30)

<223> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro; Xaa at residues 8 and 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or bromo-Trp

<400> 304

Asp Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn
1 5 10 15

Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
20 25 30

<210> 305

<211> 281

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (7)..(234)

<400> 305

ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gtt gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag 96
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac gag agg tgc ctt gaa aag ggt gta ctt tgt gat ccg agt 192
Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser
50 55 60

gct gga aac tgc tgt agt ggc gaa tgc gtt tta gtc tgc ctc 234
Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

taaaactacc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

<210> 306

<211> 76

<212> PRT

<213> Conus arenatus

<400> 306

Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser Ala Gly
50 55 60

Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

034967 084304

<210> 307
 <211> 25
 <212> PRT
 <213> Conus arenatus

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residues 3 and 19 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Pro or hydroxy-Pro

<400> 307
 Cys Leu Xaa Lys Gly Val Leu Cys Asp Xaa Ser Ala Gly Asn Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys Val Leu Val Cys Leu
 20 25

<210> 308
 <211> 287
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
 <222> (7)..(240)

<400> 308
 ggatcc atg aaa ctg acg tgc atg gtg atc gtt act gtg ttg ttc ttg 48
 Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gaa ttg gag 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu
 15 20 25 30
 aat ctt ttt ctg aag gca tat cac gaa atg aac tcc gaa gcc tct aaa 144
 Asn Leu Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys
 35 40 45
 ttg gac aag aaa gag tgc gtt gct ggt agt cac ttt tgt ggt ttt ccg 192
 Leu Asp Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro
 50 55 60
 aaa att gga ggg cca tgc tgc agt ggc tgg tgc ttt ttc gtc tgc ttg 240
 Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75
 taaacctgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag 287

<210> 309
 <211> 78
 <212> PRT
 <213> Conus arenatus

<400> 309
 Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu Asn Leu
 20 25 30
 Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys Leu Asp
 35 40 45

Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro Lys Ile
 50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

<210> 310
 <211> 28
 <212> PRT
 <213> Conus arenatus

<220>
 <221> SITE
 <222> (1)..(28)
 <223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residues
 12 and 17 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tr
 p or bromo-Trp

<400> 310
 Xaa Cys Val Ala Gly Ser His Phe Cys Gly Phe Xaa Lys Ile Gly Gly
 1 5 10 15

Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
 20 25

<210> 311
 <211> 400
 <212> DNA
 <213> Conus tessulatus

<220>
 <221> CDS
 <222> (7)..(243)

<400> 311
 ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg atg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu
 1 5 10

acc gcc tgg aca ttc atc acg gct gat gac tcc ata aat gga ctg gag 96
 Thr Ala Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
 15 20 25 30

gat aga ggc ata tgg ggg gaa cct ttg tgc aag gca cgt gac gaa atg 144
 Asp Arg Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met
 35 40 45

aac ccc gaa gtc tct aaa cgg gat tgc tgg cct caa tat tgg ttt tgt 192
 Asn Pro Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys
 50 55 60

ggc cta cag agg gga tgc tgc cca ggg act act tgc ttc ttc ctt tgc 240
 Gly Leu Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys
 65 70 75

ttt tagtgatctc ttogactccc ttctgtgcta cctggcttga cctttgattg 293
 Phe

gcgcgtgccc ttcaactggtt ataaaccct ctgttcctcc tctctggacg cttcgggggtg 353
 .
 tccagcatcc aaataaagcg acgtcccca aaaaaaaaaa aaaaaaa 400

<210> 312

09749637.001307

<211> 79
 <212> PRT
 <213> Conus tessulatus

<400> 312
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asp Arg
 20 25 30
 Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met Asn Pro
 35 40 45
 Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys Gly Leu
 50 55 60
 Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys Phe
 65 70 75

<210> 313
 <211> 26
 <212> PRT
 <213> Conus tessulatus
 <220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 7 may be Trp or bromo-Trp; Xaa at residues
 4 and 17 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Tyr,
 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
 -Tyr

<400> 313
 Asp Cys Xaa Xaa Gln Xaa Xaa Phe Cys Gly Leu Gln Arg Gly Cys Cys
 1 5 10 15
 Xaa Gly Thr Thr Cys Phe Phe Leu Cys Phe
 20 25

<210> 314
 <211> 419
 <212> DNA
 <213> Conus tessulatus

<220>
 <221> CDS
 <222> (7)..(249)

<400> 314
 ggatcc atg aaa ctg acg tgc gtg gtg gtc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu
 1 5 10
 aac gcc tgg aca ttc gcc acg gct gtt gac tcc aaa cat gca ctg gcg 96
 Asn Ala Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala
 15 20 25 30
 aaa ctt ttt atg aag gca cgt gac gaa atg tat aac ccc gat gcc act 144
 Lys Leu Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr
 35 40 45
 aaa ttg gac gat aag aga tgg tgc gct tta gat ggt gaa ctt tgt atc 192
 Lys Leu Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile

50 55 60
 ata ccg gtc att ggg tcc ata ttt tgc tgc cat ggc ata tgt atg atc 240
 Ile Pro Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile
 65 70 75
 tac tgc gtc tagttgaact gccgtgatgt cttctactcc cctctgtgct 289
 Tyr Cys Val
 80
 acccctgggtt tgatctttga ttgccctgtg cccttcaactg attatgaatc cctctgatcc 349
 tactctctga agacctcttg gggccaaca tccaaataaa gcgacatccc aaaaaaaaaa 409
 aaaaaaaaaa 419
 <210> 315
 <211> 81
 <212> PRT
 <213> Conus tessulatus
 <400> 315
 Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu Asn Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala Lys Leu
 20 25 30
 Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr Lys Leu
 35 40 45
 Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile Ile Pro
 50 55 60
 Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile Tyr Cys
 65 70 75 80
 Val
 <210> 316
 <211> 29
 <212> PRT
 <213> Conus tessulatus
 <220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydro-
 xy-Pro; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, d
 i-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
 <400> 316
 Xaa Cys Ala Leu Asp Gly Xaa Leu Cys Ile Ile Xaa Val Ile Gly Ser
 1 5 10 15
 Ile Phe Cys Cys His Gly Ile Cys Met Ile Xaa Cys Val
 20 25
 <210> 317
 <211> 408
 <212> DNA
 <213> Conus imperialis

<400> 319

Xaa Cys Arg Val Xaa Gly Xaa Ile Cys Gly Met Leu Phe Xaa Ala Gln
 1 5 10 15

Cys Cys Asp Gly Xaa Cys Phe Phe Val Cys Met
 20 25

<210> 320

<211> 281

<212> DNA

<213> Conus characteristicus

<220>

<221> CDS

<222> (7)..(234)

<400> 320

ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu
 15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45

aaa ttg aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt ccg gga 192
 Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly
 50 55 60

ttt gga gat tgc tgc act ggc ttc tgc ctt tta gtc tgc atc 234
 Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
 65 70 75

taaaactgcc gtgatgtcct ctactcccat ctgtgctacc cctcgag 281

<210> 321

<211> 76

<212> PRT

<213> Conus characteristicus

<400> 321

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly Phe Gly
 50 55 60

Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
 65 70 75

<210> 322

<211> 25

<212> PRT

<213> Conus characteristicus

094957 08404

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Glu or gamma-carboxy-Glu

<400> 322
 Cys Val Asp Xaa Gly Xaa Phe Cys Gly Xaa Gly Phe Gly Asp Cys Cys
 1 5 10 15
 Thr Gly Phe Cys Leu Leu Val Cys Ile
 20 25

<210> 323
 <211> 287
 <212> DNA
 <213> Conus miliaris

<220>
 <221> CDS
 <222> (7)..(240)
 <400> 323
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ttg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttc gtc atg gct gat gac tcc aga aat gat ttg gag 96
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu
 15 20 25 30
 aat ctt ttt ctg aag gca cgt cat gaa atg aag aac ccc gaa gct tct 144
 Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45
 aaa ttg aac aag aga tgc ctt cca aat ggt gta ctt tgt gat ctg gga 192
 Lys Leu Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly
 50 55 60
 tct cca cca tac tgc tgc agt ggc tgg tgc gcg atc gtc gtc tgc atc 240
 Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile
 65 70 75
 taaaactgtc gtcattgtctt ctactcccat ctgtgctacc cctcgag 287

<210> 324
 <211> 78
 <212> PRT
 <213> Conus miliaris

<400> 324
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu
 20 25 30
 Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly Ser Pro
 50 55 60
 Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile

65 70 75

<210> 325
 <211> 27
 <212> PRT
 <213> *Conus miliaris*

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residues 3, 13 and 14 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-Trp

<400> 325
 Cys Leu Xaa Asn Gly Val Leu Cys Asp Leu Gly Ser Xaa Xaa Xaa Cys
 1 5 10 15

Cys Ser Gly Xaa Cys Ala Ile Val Val Cys Ile
 20 25

<210> 326
 <211> 287
 <212> DNA
 <213> *Conus atlanticus*

<220>
 <221> CDS
 <222> (7)..(240)

<400> 326
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc ata aat ggg ttg gag 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
 15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg agg aaa ccc gaa gcc tct 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser
 35 40 45

aga tcg aga ggg agg tgc cgt cct cgt ggt atg ttc tgt ggc ttt ccg 192
 Arg Ser Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro
 50 55 60

aaa cct gga cca tac tgc tgc aat ggc tgg tgc ttt ttc gtc tgc atc 240
 Lys Pro Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile
 65 70 75

taaaactgcc gtgatgtgtt ctactcccat ctgtgctacc cctcgag 287

<210> 327
 <211> 78
 <212> PRT
 <213> *Conus atlanticus*

<400> 327
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu

20 25 30

Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser Arg Ser
35 40 45

Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro Lys Pro
50 55 60

Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile
65 70 75

<210> 328
<211> 27
<212> PRT
<213> Conus atlanticus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bromo-Trp

<400> 328
Cys Arg Xaa Arg Gly Met Phe Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa
1 5 10 15

Cys Cys Asn Gly Xaa Cys Phe Phe Val Cys Ile
20 25

<210> 329
<211> 284
<212> DNA
<213> Conus lividus

<220>
<221> CDS
<222> (7)..(237)

<400> 329
ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag 96
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
15 20 25 30

aat ctt ttt tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt 192
Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
50 55 60

gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta 237
Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

taaaactacc gtgatgtctt ctactcccat ctgtgctacc cctcgag 284

<210> 330

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<211> 77
 <212> PRT
 <213> Conus lividus

<400> 330
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60
 Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
 65 70 75

<210> 331
 <211> 26
 <212> PRT
 <213> Conus lividus
 <220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and
 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 ma
 y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

<400> 331
 Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
 1 5 10 15
 Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
 20 25

<210> 332
 <211> 281
 <212> DNA
 <213> Conus pulicarius

<220>
 <221> CDS
 <222> (7)..(234)

<400> 332
 ggatcc atg aaa ctg acg tgc atg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttc gtc aag gct gat gac tcc aga aat gga ttg gag 96
 Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu
 15 20 25 30
 aat ctt ttt ccg aag gca cgt cac gaa atg aag aac tcc aaa gcc tct 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser
 35 40 45
 aaa tta aac aag agg tgc gtt gaa gat ggt gat ttt tgt ggt ccg gga 192
 Lys Leu Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly

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50 55 60
 tat gaa gag tgc tgc agt ggc ttc tgc ctt tac gtc tgc atc 234
 Tyr Glu Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
 65 70 75
 taaaactgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281
 <210> 333
 <211> 76
 <212> PRT
 <213> *Conus pullicarius*
 <400> 333
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly Tyr Glu
 50 55 60
 Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
 65 70 75
 <210> 334
 <211> 25
 <212> PRT
 <213> *Conus pullicarius*
 <220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa
 at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and
 22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 r or O-phospho-Tyr
 <400> 334
 Cys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Xaa Cys Cys
 1 5 10 15
 Ser Gly Phe Cys Leu Xaa Val Cys Ile
 20 25
 <210> 335
 <211> 293
 <212> DNA
 <213> *Conus generalis*
 <220>
 <221> CDS
 <222> (7)..(249)
 <400> 335
 ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttc gtc acg gct gat gac acc aga tat aaa ctg gag 96

Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu
 15 20 25 30

aat cct ttt ctg aag gca cgc aac gaa ctg cag aaa cac gaa gcc tct 144
 Asn Pro Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser
 35 40 45

caa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg acg 192
 Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr
 50 55 60

ccg ttt ctt gga gca tac tgc tgc ggt ggc att tgc ctt att gtc tgc 240
 Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys
 65 70 75

ata gaa acg taaaggcttg atgtcttcta ctcccatctg tgctaccct cgag 293
 Ile Glu Thr
 80

<210> 336
 <211> 81
 <212> PRT
 <213> Conus generalis

<400> 336
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu Asn Pro
 20 25 30

Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser Gln Leu
 35 40 45

Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr Pro Phe
 50 55 60

Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Glu
 65 70 75 80

Thr

<210> 337
 <211> 30
 <212> PRT
 <213> Conus generalis

<220>
 <221> SITE
 <222> (1)..(30)
 <223> Xaa at residues 5 and 12 may be Pro or hydroxy-Pro; Xaa at residu
 es 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
 sulpho-Tyr or O-phospho-Tyr

<400> 337
 Gly Cys Leu Asp Xaa Gly Xaa Phe Cys Gly Thr Xaa Phe Leu Gly Ala
 1 5 10 15

Xaa Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Xaa Thr
 20 25 30

<210> 338
 <211> 400
 <212> DNA

65 70 75

<210> 343
 <211> 31
 <212> PRT
 <213> *Conus episcopatus*

<220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydroxy-Pro

<400> 343
 Gly Cys Leu Ala Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Ser Asn
 1 5 10 15
 Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
 20 25 30

<210> 344
 <211> 202
 <212> DNA
 <213> *Conus achatinus*

<220>
 <221> CDS
 <222> (85)..(171)

<400> 344
 cgatcctctg tcctccatct attattattc gctgccaaac tgtgttaaatt attcaagtct 60
 ctctttctgt ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat 111
 Leu Arg Trp Cys Ile Pro Arg Gly Asp
 1 5
 ott tgt ttc ccc tcg gat cgc ata caa tgc tgc agt ggc aag tgc aca 159
 Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr
 10 15 20 25
 ttc gtc tgc atg taaaactgcc gtgatgtctt ctctccct c 202
 Phe Val Cys Met

<210> 345
 <211> 29
 <212> PRT
 <213> *Conus achatinus*

<400> 345
 Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg
 1 5 10 15
 Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
 20 25

<210> 346
 <211> 27
 <212> PRT
 <213> *Conus achatinus*

<220>
 <221> SITE
 <222> (1)..(27)

001963 001001

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

<400> 346

Xaa Cys Ile Xaa Arg Gly Asp Leu Cys Phe Xaa Ser Asp Arg Ile Gln
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 347

<211> 202

<212> DNA

<213> *Conus achatinus*

<220>

<221> CDS

<222> (85)..(171)

<400> 347

cgatcctctg tcctcctcct tcattcattc gctgccaaac tgtattaaat attcgaatct 60

ctctttctgt ttgtgtctga caga ttg aga ggg tgc gtt cct agt ggt gaa 111
Leu Arg Gly Cys Val Pro Ser Gly Glu
1 5

att tgt tac ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca 159
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr
10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctctcccat c 202
Phe Val Cys Met

<210> 348

<211> 29

<212> PRT

<213> *Conus achatinus*

<400> 348

Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 349

<211> 27

<212> PRT

<213> *Conus achatinus*

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 349

Gly Cys Val Xaa Ser Gly Xaa Ile Cys Xaa Phe Met Asp His Ile Gly
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<400> 352

Asp Xaa Cys Ser Ala Xaa Gly Ala Phe Cys Leu Ile Arg Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Phe Ala Cys Phe
 20 25

<210> 353

<211> 276

<212> DNA

<213> Conus bullatus

<220>

<221> CDS

<222> (1)..(246)

<400> 353

atg aaa ctg acg tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga gac gct ccg gat agt gca 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
 20 25 30

gaa gga tgg gag aaa ctt ttc tgc gag gca cgt gac gaa atg aag aac 144
 Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
 35 40 45

cgc aaa gac ttt gaa ttg aga ggg tgc ctt cct agg tgg gaa ttt tgt 192
 Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
 50 55 60

ccc atc ttt aaa aaa aac gat tgc tgc agt ggc ata tgc ata agc atc 240
 Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
 65 70 75 80

tgc ttg taaaactccg tgatgtcttc tcttcccatc 276
 Cys Leu

<210> 354

<211> 82

<212> PRT

<213> Conus bullatus

<400> 354

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
 20 25 30

Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
 35 40 45

Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
 50 55 60

Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
 65 70 75 80

Cys Leu

<210> 355

<211> 27
 <212> PRT
 <213> Conus bullatus

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu

<400> 355
 Gly Cys Leu Xaa Arg Xaa Xaa Phe Cys Xaa Ile Phe Lys Lys Asn Asp
 1 5 10 15
 Cys Cys Ser Gly Ile Cys Ile Ser Ile Cys Leu
 20 25

<210> 356
 <211> 268
 <212> DNA
 <213> Conus striolatus

<220>
 <221> CDS
 <222> (1)..(237)

<400> 356
 atg aaa ctg acg tgc atg atg att gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg ata ttt gta atg gct gat gac tcc aga aat gga ttg gag aat ctt 96
 Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 cct cag act aca cgt cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac cag aca gac tgc ctt gct aaa gac gct ttc tgt gcc tgg ccg ata 192
 Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
 50 55 60
 ctt gga cca ctg tgc tgc agt cgc ttg tgc tta tac gtc tgc atg 237
 Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
 65 70 75
 taaaactgcc gtgatgtctt ctactccct c 268

<210> 357
 <211> 79
 <212> PRT
 <213> Conus striolatus

<400> 357
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
 50 55 60

Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
 65 70 75

<210> 358
 <211> 28
 <212> PRT
 <213> Conus striolatus

<220>
 <221> SITE
 <222> (1)..(28)
 <223> Xaa at residue 11 may be Trp or bromo-Trp; Xaa at residues 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

<400> 358
 Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
 1 5 10 15

Leu Cys Cys Ser Arg Leu Cys Leu Xaa Val Cys Met
 20 25

<210> 359
 <211> 266
 <212> DNA
 <213> Conus consors

<220>
 <221> CDS
 <222> (1)..(246)

<400> 359
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
 35 40 45
 aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
 50 55 60
 gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
 65 70 75 80
 ttt tcg tgatgtcttc tcctcccctc 266
 Phe Ser

<210> 360
 <211> 82
 <212> PRT
 <213> Conus consors

<400> 360

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
 35 40 45
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
 50 55 60
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
 65 70 75 80

Phe Ser

<210> 361
 <211> 31
 <212> PRT
 <213> Conus consors
 <220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 361
 Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
 1 5 10 15
 Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
 20 25 30

<210> 362
 <211> 289
 <212> DNA
 <213> Conus consors

<220>
 <221> CDS
 <222> (1)..(252)

<400> 362
 atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt 192
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
 50 55 60
 cca gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe

65 70 75 80

gtt gat tct ggc taacagtgtg cgttggttga tgtctttctac tcccctc 289

Val Asp Ser Gly

<210> 363
 <211> 84
 <212> PRT
 <213> Conus consors

<400> 363

Met	Lys	Leu	Thr	Cys	Leu	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Thr
1				5					10					15	

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu

			20					25					30		
--	--	--	----	--	--	--	--	----	--	--	--	--	----	--	--

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu

			35					40				45			
--	--	--	----	--	--	--	--	----	--	--	--	----	--	--	--

Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg

			50					55				60			
--	--	--	----	--	--	--	--	----	--	--	--	----	--	--	--

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe

			65					70				75			80
--	--	--	----	--	--	--	--	----	--	--	--	----	--	--	----

Val Asp Ser Gly

<210> 364
 <211> 32
 <212> PRT
 <213> Conus consors

<220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 364

Asp	Gly	Cys	Xaa	Asn	Ala	Gly	Thr	Phe	Cys	Gly	Ile	Arg	Xaa	Gly	Leu
1				5					10					15	

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser

			20					25				30			
--	--	--	----	--	--	--	--	----	--	--	--	----	--	--	--

<210> 365
 <211> 205
 <212> DNA
 <213> Conus circumcicus

<220>
 <221> CDS
 <222> (83)..(175)

<400> 365

cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly

			1					5						10	
--	--	--	---	--	--	--	--	---	--	--	--	--	--	----	--

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttcctc 205
 Ala Phe Val Cys Leu
 30

<210> 366
 <211> 31
 <212> PRT
 <213> Conus circumciscus

<400> 366
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15
 Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

<210> 367
 <211> 26
 <212> PRT
 <213> Conus circumciscus

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 367
 Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15
 Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 368
 <211> 206
 <212> DNA
 <213> Conus circumciscus

<220>
 <221> CDS
 <222> (83)..(175)

<400> 368
 cgatccatct gtccatccat ctattcattc attcgtgtc aaactgtatt aaatattcaa 60
 gtctctottt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
 1 5 10

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc agt gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactcccct c 206
 Ala Phe Val Cys Leu
 30

<210> 369
 <211> 31
 <212> PRT

<213> Conus circumciscus

<400> 369

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

<210> 370

<211> 27

<212> PRT

<213> Conus circumciscus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

<400> 370

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

<210> 371

<211> 206

<212> DNA

<213> Conus circumciscus

<220>

<221> CDS

<222> (83)..(175)

<400> 371

cgatccatct gtccatccat ctattcattc attcgtgtgc aaactgtatt aaatattcaa 60

gtctctcttt ctgttttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc agt gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctcccct c 206
Ala Phe Val Cys Leu
30

<210> 372

<211> 31

<212> PRT

<213> Conus circumciscus

<400> 372

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

<210> 373

<211> 26
 <212> PRT
 <213> Conus circumciscus

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 373
 Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15

Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 374
 <211> 206
 <212> DNA
 <213> Conus circumciscus

<220>
 <221> CDS
 <222> (83)..(175)

<400> 374
 cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
 1 5 10

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc gag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctccct c 206
 Ala Phe Val Cys Leu
 30

<210> 375
 <211> 31
 <212> PRT
 <213> Conus circumciscus

<400> 375
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu
 20 25 30

<210> 376
 <211> 26
 <212> PRT
 <213> Conus circumciscus

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu

<400> 376

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15

Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu
 20 25

<210> 377
 <211> 206
 <212> DNA
 <213> Conus circumciscus

<220>
 <221> CDS
 <222> (83)..(175)

<400> 377
 cgatccatct gtccatccat ctattcattc attcgctgtc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
 1 5 10

gat ctt tgt ttc ccc tcg gat cac ata cga tgc tgc agt gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttcccat c 206
 Ala Phe Val Cys Leu
 30

<210> 378
 <211> 31
 <212> PRT
 <213> Conus circumciscus

<400> 378
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15

Asp His Ile Arg Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

<210> 379
 <211> 27
 <212> PRT
 <213> Conus circumciscus

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
 1 may be Pro or hydroxy-Pro

<400> 379
 Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Arg
 1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 380
 <211> 206
 <212> DNA
 <213> Conus circumciscus

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<220>
<221> CDS
<222> (83)..(175)

<400> 380
cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60
gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
                               Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
                               1 5 10

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
                               15 20 25

gca ttc gcc tgc ttg taaaactgcc gtgatgtctt ctcttcccct c 206
Ala Phe Ala Cys Leu
                               30

<210> 381
<211> 31
<212> PRT
<213> Conus circumcisis

<400> 381
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25 30

<210> 382
<211> 26
<212> PRT
<213> Conus circumcisis

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 382
Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15

Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25

<210> 383
<211> 206
<212> DNA
<213> Conus circumcisis

<220>
<221> CDS
<222> (83)..(175)

<400> 383
cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60
gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
                               Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
                               1 5 10

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gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactccoct c 206
Ala Phe Val Cys Leu
30

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<400> 384
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1          5          10          15
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<210> 385
<211> 27
<212> PRT
<213> Conus circumcissus
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<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro
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<400> 385
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15

```
<210> 386
<211> 200
<212> DNA
<213> Conus circumcissus
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<220>
<221> CDS
<222> (77) .. (169)
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ctttctgttt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt 112
Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu
1 5 10

tgt ttc ccc tcg gat cac ata caa tgc tgc agt ggc aag tgc aca ttc 160
Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe
15 20 25

gtc tgc atg taaaaactgcc gtgatgtctt ctctctccct c 200
Val Cys Met
30

$\langle 210 \rangle$	387
$\langle 211 \rangle$	31

<213> Conus monachus

<400> 390

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

<210> 391

<211> 31

<212> PRT

<213> Conus monachus

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 391

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<210> 392

<211> 277

<212> DNA

<213> Conus stercusmuscarum

<220>

<221> CDS

<222> (1)..(246)

<400> 392

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc aca gct gat gac tcc ata aat gga ccg gag aat aga 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
20 25 30

cga ata tgg gag aaa ctt ttg ttg aag gca cgt gac gaa atg aag aac 144
Arg Ile Trp Glu Lys Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
35 40 45

ccc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt 192
Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
50 55 60

094967 0310

ttc cgc tcg gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc 240
 Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
 65 70 75 80

tgc ttg taaaactacc gtgatgtctt ctctcccat c 277
 Cys Leu

<210> 393
 <211> 82
 <212> PRT
 <213> Conus stercusmuscarum

<400> 393
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
 20 25 30

Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
 35 40 45

Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
 50 55 60

Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
 65 70 75 80

Cys Leu

<210> 394
 <211> 27
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be
 Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy
 -Glu

<400> 394
 Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Pro Arg Ser Asp His Ile Gln
 1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 395
 <211> 266
 <212> DNA
 <213> Conus stercusmuscarum

<220>
 <221> CDS
 <222> (1)..(246)

<400> 395
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg atc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg aag aat ctt 96

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cgt 192
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
 50 55 60

cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80

att gat tgatgtcttc tattcccctc 266
 Ile Asp

<210> 396
 <211> 82
 <212> PRT
 <213> Conus stercusmuscarum

<400> 396
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80

Ile Asp

<210> 397
 <211> 31
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 397
 Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
 20 25 30

<210> 398
 <211> 265
 <212> DNA
 <213> Conus striolatus

<220>

<221> CDS

<222> (1)..(234)

<400> 398

atg	aaa	ctg	acg	tgc	ata	atg	acc	gtt	gct	gtg	ctg	ttc	ttg	acc	gct	48
Met	Lys	Leu	Thr	Cys	Ile	Met	Thr	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala	
1				5					10					15		

tgg	aca	ttc	gtc	acg	gct	gat	gac	tcc	aga	aat	gga	ttg	gag	aat	ctt	96
Trp	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu	
			20					25					30			

ctt	ctg	aag	aca	cgt	cac	gaa	gtg	gaa	aac	ccc	aaa	gcc	tct	agg	tcg	144
Leu	Leu	Lys	Thr	Arg	His	Glu	Val	Glu	Asn	Pro	Lys	Ala	Ser	Arg	Ser	
		35					40					45				

ggc	ggt	agg	tgc	cgt	cct	ggt	ggt	acg	gtt	tgt	ggc	ttt	ccg	aaa	cct	192
Gly	Gly	Arg	Cys	Arg	Pro	Gly	Gly	Thr	Val	Cys	Gly	Phe	Pro	Lys	Pro	
	50					55					60					

gga	cca	tac	tgc	tgc	agt	ggc	tgg	tgc	ttt	ttt	gtc	tgc	gcc			234
Gly	Pro	Tyr	Cys	Cys	Ser	Gly	Trp	Cys	Phe	Phe	Val	Cys	Ala			
65					70					75						

taaac	cctgcc	gtgat	gtctt	ctoct	cccat	c	265
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<210> 399

<211> 78

<212> PRT

<213> Conus striolatus

<400> 399

Met	Lys	Leu	Thr	Cys	Ile	Met	Thr	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala
1				5					10					15	

Trp	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu
			20					25					30		

Leu	Leu	Lys	Thr	Arg	His	Glu	Val	Glu	Asn	Pro	Lys	Ala	Ser	Arg	Ser
		35					40					45			

Gly	Gly	Arg	Cys	Arg	Pro	Gly	Gly	Thr	Val	Cys	Gly	Phe	Pro	Lys	Pro
	50					55					60				

Gly	Pro	Tyr	Cys	Cys	Ser	Gly	Trp	Cys	Phe	Phe	Val	Cys	Ala
65					70				75				

<210> 400

<211> 27

<212> PRT

<213> Conus striolatus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bro mo-Trp

<400> 400

Cys	Arg	Xaa	Gly	Gly	Thr	Val	Cys	Gly	Phe	Xaa	Lys	Xaa	Gly	Xaa	Xaa
1				5					10				15		

Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala
 20 25

<210> 401
 <211> 272
 <212> DNA
 <213> Conus striolatus

<220>
 <221> CDS
 <222> (1)..(243)

<400> 401
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30
 ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45
 gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
 65 70 75 80
 ggt taactgccgt gatgtcttct attcccctc 272
 Gly

<210> 402
 <211> 81
 <212> PRT
 <213> Conus striolatus

<400> 402
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
 65 70 75 80
 Gly

<210> 403
 <211> 29
 <212> PRT
 <213> Conus striolatus

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<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 403
 Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
 20 25

<210> 404
 <211> 265
 <212> DNA
 <213> Conus striolatus

<220>
 <221> CDS
 <222> (1)..(246)

<400> 404
 atg aaa ctg acg tgt ctg atg gct gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 cgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96
 Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
 35 40 45
 aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
 50 55 60
 gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
 65 70 75 80
 ttt tcg tgatgtcttc tatccctc 265
 Phe Ser

<210> 405
 <211> 82
 <212> PRT
 <213> Conus striolatus

<400> 405
 Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
 35 40 45
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn

50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

<210> 406
<211> 31
<212> PRT
<213> Conus striolatus

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 406
Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<210> 407
<211> 287
<212> DNA
<213> Conus striolatus

<220>
<221> CDS
<222> (1)..(231)

<400> 407
atg aaa ctg acg tgt atg gtg atc gtc gcc gtg ctg ctc ctg acg acc 48
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15

tgt cat ctc atc aca gct gat gac tcc aga ggt acg cag aag cat cgt 96
Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

tcc ctg agg tcg act acc aaa gtc tcc aag tcg act agc tgc atg aaa 144
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

gcc ggg tct tat tgc gtc gct act acg aga atc tgc tgc ggt tat tgc 192
Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
50 55 60

gct tat ttc ggc aaa ata tgt att ggc tat ccc aaa aac tgatcctccc 241
Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
65 70 75

cctactgtgc tctatccttt tctgcctgat gtctttctcct cccctc 287

<210> 408
<211> 77
<212> PRT
<213> Conus striolatus

<400> 408

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15

Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
65 70 75

<210> 409

<211> 35

<212> PRT

<213> Conus striolatus

<220>

<221> SITE

<222> (1)..(35)

<223> Xaa at residues 10, 21, 24 and 32 may be Tyr, 125-I-Tyr, mono-iod
o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue
33 may be Pro or hydroxy-Pro

<400> 409

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Gly Xaa
20 25 30

Xaa Lys Asn
35

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